

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: David William Holden
- (ii) TITLE OF INVENTION: Identification of Genes
- (iii) NUMBER OF SEQUENCES: 501
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Patrea L. Pabst
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1201 West Peachtree Street
  - (C) CITY: Atlanta
  - (D) STATE: Georgia
  - (E) COUNTRY: USA
  - (F) ZIP: 30309-3450
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 01-DEC-1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/637,759
  - (B) FILING DATE: 03-MAY-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/GB95/02875
  - (B) FILING DATE: 11-DEC-1995
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Pabst, Patrea L.
  - (B) REGISTRATION NUMBER: 31,284
  - (C) REFERENCE/DOCKET NUMBER: RPMS 101 CON 2
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (404) 873-8794
  - (B) TELEFAX: (404) 873-8795

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTAGGTACCT ACAACCTCAA GCTTNKNKNK NKNKNKNKNK NKNKNKNKNK NKNKNKNKNK

60

NKNKAAGCTT GGTTAGAATG GGTACCATG

89

- (2) INFORMATION FOR SEQ ID NO: 2:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Synthetic oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TACCTACAAC CTCAAGCT

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- (2) INFORMATION FOR SEQ ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Synthetic oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CATGGTACCC ATTCTAAC

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- (2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Synthetic oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TACCCATTCT AACCAAGC

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- (2) INFORMATION FOR SEQ ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTAGGTACCT ACAACCTC

18

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCTAGGCGGC CAGATCTGAT

20

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCACTTGTGT ATAAGAGTCA G

21

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Partial sequence of Salmonella typhimurium  
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGTCTTAATG TACGGGCATG GTCTGCATCG ATAACTCCGG CACGCAAATC GCCATCGATA

60

CTCATTGTGTT TGGCTGGCAT CCCATCAAGC GAGAAACGTG CGCTAACTTC CGCCACCCTC

120

TCGATACCTT TTGTAATGAC AATAAATTGC ACGATAGTAA TGATGGTAAA TACGACCAAC 180  
 CCAACGGTGA GATTTCTCTCC TACGACAAAC TTACCGAAAG CATCCACAAA TATTACCGGC 240  
 ATTATGTTGT AACAGTACCC AGCCGTGATG TGCTGATTGG GGAGTTAACA ACCGATTTAT 300

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCGCGGACGC TAGTGTGGTG GGTGACAGCC AGACGTTACC GAACGGGATG GGGCAGATCT 60  
 GTTGGCTTAC AAAAGACATG GCCCATAAGG CGCAAGGTTT TGGGACTGGA CGTTTTCGCG 120  
 GGCAGACAAC GTATCTCTGT CTTATTAAAA TGTGTCCTGC TTCGGCATAT GTATCGAACC 180  
 CTCGGAGCAA AGTCGTTTGG GCGCAGAATT AGTACGTTTG GGTCCGTTGC TGTTATTCCT 240  
 TGGGCTCGGA AAAAGAGTGC CAGCGTGAAG GAGTGGGATT TGGCAGACTG GCCGCCTAAT 300

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CACTATAGGG AAAGCTTGCA TGCCTGCAGG TCGACTCTAG AGGATCTACT AGTCATATGG 60  
 ATTGCACTTG TGTATAAGAG TCAGGATTAG AGGACATGCG CCGGGAACCA TACTATCTTT 120  
 TTCCGGTGCT TCGACGCCAT TTGCGGAAAC CACAGACTTT TTGCGGCGAA TGAGGATAAT 180  
 TGGCAATGCT AACAACGCTG AAAAGAAAGC GAGAGTGATA AAAGGAAAGC CAGGAATTAA 240  
 AGCGAGGAGC ATTAAAACCA CAGCGGCTAA TATGAGCGAC TGAGGTTGTC TGGCAATTTG 300

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 300 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGCAGGCCGA CTCTAGAGGA TCCCCGGGTA CCGGTAATTT CTTTAACCTC GCATCCCCGGT	60
GGATGAAAGG ATATTCTGGC TGCCTAAGTA ATGAATGAAC CGCCAGTAG ATAAATATT	120
GAAAGTGATA ACCTGATGTT TTAATAACGA TGCAGGATAT ACATATAACA TGCTGGCATC	180
AAACCAGGTA AGCAAATCAT ATTGTGCTGC CAGGTTATTC AAATATCGA CCGGTGGTCC	240
AGGCGGGAAT TTTTCCACTA AATGTAGGTG GGATCAATGG GCTAATTGGT ATAGGCGGAT	300

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 324 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTGTGATTC CGGATGAAAT AGCTTTTACG AAAGCTGTCA GACNTGCTGA AGAATACGCT	60
GCAAATGGTA AGCTTGTAAC TTTTGGGTAT TGTTCACACG CATGCTGAAA CGGGTTATGG	120
ATATATTCGT CGCGGTGAGT TGATAGGAAA TGACGCTTAT GCAGTGGCTG AATTTGTGGA	180
GAAACCGGAT ATCGATACCG CCCGTGACTA TTTCAAATCA GGGGAAATAT TACTGGCCTA	240
GCGGCGATGT TTTTATTTTCG CGCAAAGCCC TTATTTAAAC GAATTAAACG TATCTATCAC	300
CCCCAAATTC ATACAGCTTG TGAA	324

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 292 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

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      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Partial sequence of Salmonella typhimurium
                  virulence gene

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

(2) INFORMATION FOR SEO ID NO: 14:

TTTCCTTGCC	GTGACAGTCC	GGGATGCGAG	GTTAACGAAA	TTACCGGCAC	CAAAGCTGTG	60
GAGGTGAGCG	GTGTCCCCAG	CTGCCTGACT	CGTATTAGTC	AATTAGCTTC	AGTGCTGGAT	120
AATGCGTTAA	TCAAACGAAA	AGACAGTGCG	GTGAGTGTA	GTATATACAC	GCTTAAGTAT	180
GCCACTGCGA	TGGATACCCA	GTACCATTAT	CGCGATCAGT	CCGTCGTGGT	TCCAGGGGTC	240
GCCTAGTGTA	TTGCGTGAGA	TGAGTAACAC	CAGCGTCCCG	ACGTCATCGA	CGAACAATGG	300

(2) INFORMATION FOR SEQ ID NO: 15:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATGAGTAAC CTACCCAAC TGAATCTTTA CCAATATGCA TCATAATCTT CTGCTGGTAA 60  
ATGATTGGTA ATATCGGAAA GGTAAGTGAC ATAAGCACGC CATTACGTAA AAGTGCGGCC 120  
CCTAAACTGC CACTTTTTAA TAAGGGAAGT AATAAAGAAA GGCTCAATGG TCGAATAAAA 180  
GCCACAGCCA ATGCAATAAG CCACTCATTT ACCTGTTGTG CCATTCAACC ATGCTCTCCA 240  
ATTTCGTAACA TTATCTGCCG GGTATAATTC AACAGGATAC CGCTAAGCCA TGGGTAG 297

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 184 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATTCCAGCCC CCGGGCCATC TAACCACTAT GAACAATCAT CTTCTGGGTG GACAATCATT 60  
GGTACCATCG GCCAGGCTTG TGCAATATGT ATGTCATCAC GTAAAAGCGC GGCCCCTTAA 120  
TCTCCCCATT CTTCTTAAG GGCAGTTATC ACGGCTGGCT CAATGGCCGG CTTAACAGCC 180  
ACAG 184

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GAGGCGCGTC TTCGGTTGAG GGTCGCCCTC CAGATCTTTA TGCTCCTGTT TTACGTCATC 60  
TTTACTCATT TTAAGATCTT TTCTAATCTT ATAATATTGA AAAGAATAGT CCAGTATGCC 120  
AACGACGAAA TAAAGAAACA TCACCCCAAC CCATAACCAT TTTTCAATG ATGAAAGCAC 180

AAGCACGCCA CAGGCTACAC CACAGCCCGG AGGGGGCCGG AAAGTGCTGG GATCTTGATT	240
AATGAAAAAG GCAAAGGGAA GAGATAGGAT GATGCATGCT GGTGAGGC AGATTATTCA	300
TCTTCG	306

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium  
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AGTTGCCGTA TTTATTAAAT ATTCACCTCA GGTCAATATG GAGGTCTTCC CGGCTAAAAA 60

TCATTGCTTT ACTAGAGATA TCACTCCCTG GGTGCAATA CAGTACGATT AGTTATCTTG 120

ATGCAGCCTG CTGATTTTCAG AATGGCAGCT GACGTACCCG CGAGACAAAC ATTCTGGATT 180

ATGGACGTTA TCAACGCCAA TATAGGGAAG GTGGTGAAGT GGTTGATGAA ATACCCCTAT 240

CCCTTG CATG TTATCGCTGA CAGGACTGTT ATCAGGAGCG GGCATCCTCG ATCGGCT 297

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium  
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CAAGAGACAG ATCCAAC TCG GGCCGATCGC CATAACGCCA GCAGTTTGAA AGATGAAAGC 60

CCAGCTTATC CAGCCATTCC GGTACAGCGT AACGAGCAGG TTGCCAGAAA TAACGATAAA 120

GTTGCAACAC CTCGGGATCA GGTCGGCTCA AAAACGGGGT CTCAGGCAAA AATAGCCGAT 180

CAGGATGCCC ACTCCTAATA ACAGTCCTGT CAACGATAAC ATCAACGGAT AAGGGTATTT 240

CATCAACCAC TTCACCACCT TCCCTTTATT GGC GTTGGAT AACGTCCATA ATCCAGA 297

(2) INFORMATION FOR SEQ ID NO: 20:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 298 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AGGGCTTTAT TGATTCCATT TTTACACTGA TGAATGTTCC GTTGCGCTGC CCGGATTACA	60
GCCGGATCCT CTAGAGTCGA CCTGCAGAAC CGAGCCAGGA GCAAATTAAT TTTTTTGGGC	120
AATTGCTGAA AGATGAAGCA TCCACCAGTA ACGCCAGTGC TTTATTACCG CAGGTTATGT	180
TGACCAGACA AATAGATTAT ATGCAGTTAA CGGTAGGCGT CGATTATCTT GTCAGAATAT	240
CAGGCGCAGC ATCGCAAGCG CTTAATAAGC TGGGTAACAT GGCATGAAGG GGCAACCC	298

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 298 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CACTATAGGG AAAGCTTGCA TGCCTGCAGG TCGACTCTAG AGGATCTACT AGTCATATGG	60
ATTCTTAGGC GGCCAGATCT GATCAAGAGA CAGATCCAAC TCGGGCCGAT CGCCATAACG	120
CCAGCAGTTT GAAAGATGAA AGCCCAGCTT ATCCAGCCAT TCCGGTACAG CGTAACGAGC	180
AGGTTGCCAG AAATAACGAT AAAGTTGCAA CACCTCGGGA TCAGGTCGGC TCAAAAACGG	240
GGTCTCAGGC AAAAATAGCC GATCAGGATG CCCACTCCTA ATAACAGTCC TGTC AACG	298

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CGCCCTAGCA TGCCTGGCGT TGTCCGGTTA TTGCTCGTCA AGCGAACAGA TGCAAAAGGT 60  
GAGAGCGACT CTCGAATCAT GGGGGGTCAT GTATCGGGAT GGTGTAATCT GTGATGACTT 120  
ATTGGTACGA GAAGTGCAGG ATGTTTTGGA TAAAAATGGG TTACCCGCAT GCTGAAGTAT 180  
CCAGCGAAGG GCCGGGGAGC GTGTTAATTC ATGATGATAT ACAAATGGAT CAGCAATGGC 240  
GCAAGGTTCA ACCATTACTT GCAGATATTC CCGGGTTATT GCACTGGCAG ATTAGTCACT 300  
CTC 303

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 300 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCCTTCCCAG GCTCGACAGG TACACAGCCA GCCACTGGTG CAGGCAGTTA CTTGCTTTCA 60  
TCATGGGAAG GAGCAATATC CTGATATATT AAAGAAAGAG CGGGATCCCC TTTCTTTACT 120  
GCTGCTAACG TTTCTTGCAA AATGCGTTGA TGAGATTCAT CCAGCACACC ACTGATAACA 180  
AAAGAGCGCC GCATTGGCGT AACATTGACA AGCCCCACTA AACCGCTCTC TATTATCGCA 240  
GAAATAATAT CATCCCCCTG AGACTGATGA GAGTGACTAT TCTGCCAGCG CAAATAACCC 300

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 303 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATACCGAGTA TTAAGCGGCT GTGTAACATC GTCATCCAAC AACATACGCA GCGAGCCGCC 60  
ACGCCGAAA AACCGCATCG TGTCATGTGC CTGTTGTAGG GTCGGGTCTT TTTTCATGAG 120

TACGTTTTCT	GCGCTATCAT	ACTGGAAATT	TCCCCCAC <sup>t</sup>	TACTGATAAG	CCCTGTCAGT	180
TGGGTAAGGA	CAGAGTTAAG	CTCCTGAGAC	ATTTTTTTGGA	ATGGTTATCT	TTCCCCGACT	240
CATAAAATCG	GTATTCCCGC	TGGGGGCAAT	ATCCAAAGAC	GCTTTGGTCG	CCCGTAGGGC	300
ACC						303

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium  
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GCCGTATGCC	TGCAGTTGCC	CGGTTATTGC	TCGTCAAGCG	AACCGATGCC	AAAGGTGAGA	60
GCGACTCTCG	AATCATGGGG	GGTCATGTAT	CGGGATGGTG	TAATCTGTGA	TGACTTATTG	120
GTACGAGAAG	TGCAGGATGT	TTTGGTAAAA	ATGGGTTACC	CCCATGCTGA	AGTATCCAGC	180
GAAGGGGCGG	GGAGCGTGTT	AATTCACGAT	GATATTCAAA	TGGGTCAGCA	ATGGGGCAAG	240
GTTCAACCCC	CAC TTGCAGA	TAT TCCCCC	CCTATTGGAC	TGGCAGATTA	GTC ACTCTCA	300

(2) INFORMATION FOR SEO ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
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- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium  
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| GGGCGACCTG | CCCGCGGCGC  | AACTTTCCCC  | GAAGCGTTTT | CCATTTCCCTT | GTTCTTAAAT | 60  |
| GACCTGGAAA | GC'TTACCTAA | GCCTTGTC'TT | GCCTATGTGA | CAATACTGCT  | TGGAGAACAC | 120 |
| CCGGACGTCC | ATGATTATGC  | TATACAGATC  | ACAGCGGATG | GGGGATGGTG  | AATCGGTTAT | 180 |
| TATACCACAA | GTCGCAGCTC  | TGAGCTTATT  | GCTATTGAGA | TAGAAAAACA  | CCCCGCTTCA | 240 |

ACTTGGATTT TGAATAATGT AATACGCAAT CACCATACAC TATATTCGGG TGGCGTATAA 300

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTCTGAGCTGG GGCACCGCTA ATATCTTTAA CCTCGCATCC CGGTGATGAA AGGATATTCT | 60  |
| GGCTGCGTAA GTAATGAATG AACCGCCCAG CAGATAAAAT ATTGACAGTG ATAACCCGAT  | 120 |
| GTTTTTTTAA CGATGCAGGC TATACATATA ACATAGCTGG CCACCAACAC AGCTGAAAGTA | 180 |
| AATCATATTG TTGCTGCCAG GCTACTTCAC ACTATTGTCC GGCAGGCCAG CGGGGATTTT  | 240 |
| CCCCCTAAAT CTCGCTGGTT CTCAAA                                       | 266 |

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGTCTACGAT TTCGCTATAT CTTCTCTTAA TCATGGCCGC CATTTGTGGA TGCGATTTTA | 60  |
| AAATATCCGG GCGATCTTTC ATTAAAAAAT AAAGATTCCC CATGACTTCA CAGATAAAGG | 120 |
| TATCGGTATT TTGAGTGATA CGTAACAATT CGTTCTCTTC GTGTGGGTCC ATGATGCGAA | 180 |
| GAATAATGGT GGCATCATTT TCATGAGGAT TATGAACCCG AAATCTTTCT CTTTGCGATG | 240 |
| CGCAGGCTAA CTCTTTCAAC TCAAAAAAAA TCTCTGTAAG CCGCTCTCGT GTGGGGGCGC | 300 |

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GCGCCCCTTT AATTGGTTGA GCGGCTGGT ATTCTTGTA GGGTAATACT AGCGAGACCC    | 60  |
| AGGTTCCACC CCCGGGGACA CTTTTTAGTG TCAGATTACC GCCCATCATT TTAGCCAGGC  | 120 |
| TTGACGCAAT AGTCAGTCCA ATTCCTGTAC CTTGCGAATT TGTGTCTGCT TGATAAAAAAG | 180 |
| CAGAAAAGAT TTGAGACTGC TGCTGTTTTT CAATCCCCC ACCGCTATCG CTAACCAGAA   | 240 |
| ATATTAATTG TTCCTACCA AGATTGAGCG CCAGACGTAT CCCTCCCCC TCGGGAAAT     | 299 |

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGATAAGATC CCGGATAAGT ATGTCAGGCT CGTATGCACA ACAGGCATTA TAAACCTCTA | 60  |
| GACCATTTTT AACATGCTCT ACTATTTTAA AATGAGGCCA GGGTAATAAG GCATTCATAA | 120 |
| TGCCGTTAAT GATGATTCA TGATCGTCTA CTAATAAGAT CTTATATTCT TTCATTTGGC  | 180 |
| TGCCCTCGCG AAAATTAAGA TAATATTAAG TAATGGTGTA GGTGTGGAG ATCATACGTA  | 240 |
| TTTTCTGGCG TAAGTCGGTT AGTTCCTCCA GCGCGATGAT TTTCCCCATT TTTACGCGAT | 300 |

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 278 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCCATATTG CTCGTCCGGG GAGCGTGTTA ATTCTTGATG ATATACCAAT GGATCTGCAA 60  
TGGCGCAAGG TTCAACCATT ACTTGAGAT ATTCCCGGGT TATTGTACTG GGAGATTAGT 120  
CACTCTCATC AGTCTCAGGG GGGTGATGTT ATTTCTGGGA TAATAGAGCA ACGGCGTTAG 180  
CAGGGGTCGG TCAGTAGTCA CGGCCAACTT CGGTGCACTT TTGCGTATCA CTGGGGTATC 240  
ATAACTGAAT CTCATCCCCC CCACTTTGGT AATCACAC 278

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AATTCTTTTA CCTCCATAAG CTGCGTGGCA TAGCGATACA GAGTATTAAG CGGGTGTGTT 60  
ACATCGTCAT CCAACAACAT ACGCAGCGAG CCGCCACGCC GGAAAAACCG CATCGTGTCA 120  
TGTGCCTGTT GTAGGGTCGG GTCTTTTTTTT CATGAGTACG TGTTCTGCGC TATCATACTG 180  
GAAATTTCCC CCCACTTACT GATAAGCCCT GTCAGTTGGG TAAGGACAGC GTTAAGCTCC 240  
TGAGACATTT TTTGAGTTGT TATCTGCCCC CCGACTCATA AGATCGGGTA TTCCGCGGTG 300  
G 301

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 297 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATATCCCTAA TGCTTTTCCT TAAAATAAAT ACCACGGAAG GATACTGGCC ACCTAGCCAA 60

ATTTAGAAAG CAATGAACAT CCGGTTTATT CCTGAAAACG ATTACTCCGG CGCACGTTGT 120  
TCTGGCGTTA CCTGAGCCAG CAAACGATAT AATGGGGTGG TGACCCGCAT ACCGGTCATT 180  
GGCATCCCAT CCACACCGGA GGGAGTAAAA CTCATTAGGC CATAGGTAAT ATCATTAAGA 240  
CGCTCTAATA AATGAGGGTG GGGGGCCCAA ACTACCACTC CAGTATGTAT TGAGTCA 297

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CCCATGGGCG CAATTTGTTG CGCAGCGTTT ACCCGACCAT CGCGTTTATG AGCTGTAATT 60  
CATGGGGGGT AAAAACGGGC GTGACGACCC CAACGGAAGA TAAGGCCGGG CTTAAACAGG 120  
AGATTATTGC TAATGCGCAG CGCAAAGTGT TGCTGGCGGA CAGCAGTAAG TATGGCGCGC 180  
ATTCGCTCTT TAATGTGGTG CCGCTTGAGC GCTTTAATGA CGTGATTACC GACGTCAATC 240  
TGCCGCCGTC AGCGCAGGTT GAACTGAAAG GGCGCGCTTT TTGCGCTAAC G 291

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: DNA sequence of VGC II from centre to left hand end

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CTGCAGAACC GAGCCAGGAG CAAATTAATT TTTTGAACA ATTGCTGAAA GATGAAGCAT 60  
CCACCAGTAA CGCCAGTGCT TTATTACCGC AGGTTATGTT GACCAGACAA ATGGATTATA 120  
TGCAGTTAAC GGTAGGCGTC GATTATCTTG CCAGAATATC ACGGCGCAGC ATGCCAAGCG 180  
CTTAATAAGC TGGATAACAT GGCATGAAGG TTCATCGTAT AGTATTTCTT ACTGTCCTTA 240  
CGTTCTTTCT TACGGCATGT GATGTGGATC TTTATCGCTC ATTGCCAGAA GATGAAGCGA 300



|            |            |             |             |            |            |      |
|------------|------------|-------------|-------------|------------|------------|------|
| ATCAAATGCT | GGCATTACTT | ATGCAGCATC  | ATATTGATGC  | GAAAAAAAC  | AGGAAGAGGA | 360  |
| TGGTGTAACC | TTACGTGTCG | AGCAGTCGGC  | AGTTTATTAA  | TGCGGTTGAG | GCTACTTAGA | 420  |
| CTTAACGGTT | ATCCGCATAG | GGCAGTTTAC  | AACGGCGGAT  | AAGATGTTTC | CGGCTAATCA | 480  |
| GTTAGTGGTA | TCACCCCAGG | AAGAACAGGC  | AGAAGATTAA  | TTTTTTAAAA | GAACAAAGAA | 540  |
| TTGAAGGAAT | GCTGAGTCAG | ATGGAGGGGC  | GTGATTAATG  | GCAAAAGTGA | CCATTGCGCT | 600  |
| ACCGACTTAT | GATGAGGGAA | GTAACGCTTC  | TCCGAGCTCA  | GTTGCCGTAT | TTATAAAATA | 660  |
| TTCACCTCAG | GTCAATATGG | AGGCCTTTTCG | GGTAAAAATT  | AAAGATTTAA | TAGAGATGTC | 720  |
| AATCCCTGGG | TTGCAATACA | GTAAGATTAG  | TATCTTGATG  | CAGCCTGCTG | AATTCAGAAT | 780  |
| GGTAGCTGAC | GTACCCGCGA | GACAAACATT  | CTGGATTATG  | GACGTTATCA | ACGCCAATAA | 840  |
| AGGGAAGGTG | GTGAAGTGGT | TGATGAAATA  | CCCTTATCCG  | TTGATGTTAT | CGTTGACAGG | 900  |
| ACTGTTATTA | GGAGTGGGCA | TCCTGATCGG  | CTATTTTTCG  | CTGAGACGCC | GTTTTTGAGC | 960  |
| CGACCTGATC | CCGAGGTGTT | GCAACTTTAT  | CGTTATTTCT  | GGCAACCTGC | TCGTTACGCT | 1020 |
| GTACCGGAAT | GGCTGGATAA | GCTGGGCTTT  | CATCTTCAAA  | CTGCTGGCGT | TATGGCGATC | 1080 |
| GGCCCGAGTT | GGATCGTCTT | CTTGACAGAG  | CGTTAAATAG  | ACTAAGAGGA | AGCTCTGTTA | 1140 |
| TTCCAGCCTG | TTTAAATGAC | AGGCAAAAAC  | GGCAGGTTTCG | TCTTGCGCCG | CGTATATCGG | 1200 |
| CATTTGCCTT | TGGGCTGGGA | TTATTCAAAC  | TCAGGTGTAG  | TGACTATTTT | ATGCTACCAG | 1260 |
| AGTATCGGCA | ATTGCTTCTA | CAGTGGTTTA  | GCGAGGATGA  | GATCTGGCAG | CTATATGGTT | 1320 |
| GGTTGGGGCA | AAGAGATGGC | AAATTACTTC  | CTCCGCAAGT  | GATGCAACAA | ACTGCATTGC | 1380 |
| AGATCGGTAC | CGCCATTCTT | AATCGGGAAG  | CGCATGACGA  | TGCGGGTTTT | ACATGCGCTA | 1440 |
| TTAGTATTAT | TACCCCTCC  | GCAGCGTATA  | CTTTGGCCGA  | AGACTTCTCT | TACCGAGATT | 1500 |
| ATCTTCATGG | AGCATTTGCT | ATGAGTTTTA  | CTTCACTTCC  | TCTGACGGAA | ATTAACCATA | 1560 |
| AGCTACCCGC | TCGAAATATT | ATTGAGTCAC  | AGTGGATAAC  | ATTACAATTA | ACTTTATTTG | 1620 |
| CGCAAGAGCA | ACAAGCTAAG | AGAGTTTCAC  | ATGCTATTGT  | GAGCTCCGCT | TACCGTAAGG | 1680 |
| CTGAAAAAAT | CATCCGAGAC | GCCTATCGTT  | ATCAGCGTGA  | ACAGAAAGTT | GAGCAGCAAC | 1740 |
| AAGAAGTAGC | GTGCTTGCGT | AAAAATACGC  | TGGAAAAAAT  | GGAAGTGGAA | TGGCTGGAAC | 1800 |
| AGCATGTAAA | ACATTTACAA | GACGATGAAA  | ATCAATTTTCG | TTCATTGGTC | GATCACGCAG | 1860 |
| CGCATCATAT | TAAAAATAGT | ATAGAACAGG  | TTCTGTTGGC  | CTGGTTCGAC | CAACAGTCGG | 1920 |
| TAGACAGTGT | TATGTGCCAT | CGTCTGGCAC  | GCCAGGCCAC  | GGCTATGGCG | GAAGAGGGAG | 1980 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| CGCTTTATTT | GCGTATTCAT | CCTGAAAAAG | AGGCATTGAT | GCGAGAAACT | TTTGGCAAGC | 2040 |
| GGTTTACGTT | GATTATCGAG | CCTGGTTTCT | CTCCCGATCA | GGCTGAACTT | TCCTCAACAC | 2100 |
| GATATGCCGT | TGAATTTTCA | CTTTCTCGTC | ATTTCAACGC | GTTACTGAAA | TGGTTACGTA | 2160 |
| ATGGTGAAGA | TAAAAGAGGT | AGCGATGAAT | ATTAAAATTA | ATGAGATAAA | AATGACGCCC | 2220 |
| CCTACAGCAT | TTACCCCTGG | CCAGGTTATA | GAGGAACAAG | AGGTTATTTT | GCCTTCAATG | 2280 |
| TTAGCTCTCC | AGGAGTTACA | GGAAACGACG | GGGGCAGCGC | TCTATGAGAC | GATGGAAGAA | 2340 |
| ATAGGAATGG | CGCTGAGTGG | TAAACTGCGC | GAAAATTATA | AATTCACTGA | TGCTGAGAAA | 2400 |
| CTGGAGCGCA | GACAGCAGGC | TTTGCTGCGT | TTGATAAAAC | AAATACAGGA | GGATAATGGG | 2460 |
| GCAACGTTGC | GTCCGCTTAC | CGAAGAGAAT | AGTGATCCTG | ATTTACAGAA | TGCGTATCAA | 2520 |
| ATTATCGCTC | TTGCAATGGC | GCTTACTGCC | GGCGGGTTGT | CAAAAAAGAA | AAAACGCGAT | 2580 |
| TTGCAATCGC | AACTGGATAC | GTTACAGCGG | AGGAGGGATG | GGAACCTGCC | GTTTTTAGTT | 2640 |
| TACTGGAACT | TGGCGAAGTG | GATACCGTAC | GCTGTCTCTT | CTGAAGCGTT | TTATGCAACA | 2700 |
| GGCGATAGAC | AACGATGAAA | TGCCCTTATC | GCAGTGGTTC | AGACGCGTGG | CAGACTGGCC | 2760 |
| GGATCGCTGT | GAACGGGTCC | GTATTTTGCT | AAGAGCAGTA | GCCTTTGAAC | TTAGCATATG | 2820 |
| CATCGAACCC | TCGGAGCAAA | GTCGTTTGGC | CGCAGCATTA | GTACGTTTGC | GTCGTTTGCT | 2880 |
| GTTATTCCTT | GGCCTTGAAA | AAGAGTGCCA | GCGTGAGGAG | TGGATTTGCC | AGTTGCCGCC | 2940 |
| TAATACATTA | CTGCCGCTAC | TACTCGATAT | TATTTGTGAG | CGCTGGCTTT | TCAGTGATTG | 3000 |
| GTTGCTTGAT | AGACTTACCG | CTATAGTTTC | TTCATCGAAG | ATGTTCAATC | GGTTACTCCA | 3060 |
| ACAACCTGAT | GCGCAGTTTA | TGCTGATACC | CGATAACTGT | TTTAACGACG | AAGATCAACG | 3120 |
| TGAACAAATT | CTCGAAACGC | TTCGTGAAGT | AAAGATAAAT | CAGGTTTTAT | TCTGATACCT | 3180 |
| GGCTTTCAAT | ATTTAGGTAA | ATTGGCTTTC | TGGCTCATCA | TGAGGCGTCA | GGATGGATTG | 3240 |
| GGATCTCAT  | ACTGAACGTA | ATATTCAGCT | TTTTATTCAA | TTAGCAGGAT | TAGCTGAACG | 3300 |
| GCCTTTAGCA | ACCAATATGT | TCTGGCGGCA | AGGACAATAT | GAAACTATCA | TAACGGTCGT | 3360 |
| ATTCTCTTAT | GTCAGATACT | CAAGCAAACC | TTCTTAGACG | AAGAACTGCT | TTTTAAAGCG | 3420 |
| TTGGCTAACT | GGAAACCCGC | AGCGTTCAG  | GGTATTCCTC | AACGATTATT | TTTGTTGCGC | 3480 |
| GATGGGCTTG | CAATGAGTTG | TTCTCCACCT | CTTTCAGCT  | CCGCCGAGCT | CTGGTTACGA | 3540 |
| TTACATCATC | GACAAATAAA | ATTTCNTGGA | GTCGCAATGC | GTTTATGGTT | AGGTGAGGGA | 3600 |
| GTCAGGGCGC | AACAGTGGCT | CAGTGTATGC | GCGGGTCGGC | AGGATATGGT | TCTGGCGACG | 3660 |
| GTGTTATTAA | TCGCTATTGT | GATGATGCTG | TTACCTTGTC | CGACCTGGAT | GGTTGATATC | 3720 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| CTGATTACTA TCAACCTTAT GTTTTTCAGTG ATCCTGCTCT TAATTGCTAT TTATCTTAGT | 3780 |
| GACCCTCTCG ATTTATCGGT ATTTCCGTCT TTATTACTTA TTACTACATT ATATCGTTTG  | 3840 |
| TCACTCACAA TCAGCACATC ACGGCTGGTA CTGTTACAAC ATAATGCCGG TAATATTGTG  | 3900 |
| GATGCTTTTCG GTAAGTTTGT CGTAGGAGGA AATCTCACCG TTGGGTTGGT CGTATTTACC | 3960 |
| ATCATTACTA TCGTGCAATT TATTGTCATT AAAAAAGGTA TCGAGAGGGT GGCGGAAGTT  | 4020 |
| AGCGCACGTT TCTCGCTTGA TGGGATGCCA GGCAAACAAA TGAGTATCGA TGGCGATTTG  | 4080 |
| CGTGCCGGAG TTATCGATGC AGACCATGCC CGTACATTAA GACAGCATGT CCAGCAGGAA  | 4140 |
| AGCCGCTTTC TCGGTGCGAT GGACGGTGCG ATGAAATTTG TTAAAGGCGA TACGATTGCC  | 4200 |
| GGTATTATTG TTGTTCTGGT GAACATTATC GGCGGTATCA TTATCGCTAT CGTACAATAT  | 4260 |
| GATATGTCGA TGAGTGAGGC TGTTCACACT TATAGCGTAC TGTCAATCGG AGATGGTTTA  | 4320 |
| TGTGGGCAAA TTCCATCGCT GCTGATTTCC CTTAGCGCGG GAATTATTGT CACCCGTGTC  | 4380 |
| CCGGGTGAGA AACGCCAGAA CCTGGCGACA GAGTTGAGTT CTCAAATTGC CAGACAACCT  | 4440 |
| CAGTCGCTCA TATTAACCGC TGTGGTTTTA ATGCTCCTCG CTTTAATTCC TGGCTTTCCT  | 4500 |
| TTTATCACTC TCGCTTTCCT TTCAGCGTTG TTAGCATTGC CAATTATCCT CATTCGCCGC  | 4560 |
| AAAAAGTCTG TGGTTTCCGC AAATGGCGTC GAAGCACCGG AAAAAGATAG TATGGTTCCC  | 4620 |
| GGCGCATGTC CTCTAATCTT ACGTCTTAGC CCGACGTTAC ATTCTGCCGA CCTGATTTCG  | 4680 |
| GATATTGACG CCATGAGATG GTTTTTATTT GAGGATACCG GCGTCCCTCT CCCTGAGGTG  | 4740 |
| AATATTGAGG TTTTGCCTGA ACCCACCAGAA AAATTGACGG TACTGCTATA TCAGGAACCC | 4800 |
| GTATTTAGTT TATCTATTCC CGCTCAGGCG GATTATTTAT TGATAGGCGC GGACGCTAGT  | 4860 |
| GTGGTGGGTG ACAGCCAGAC GTTACCGAAC GGGATGGGGC AGATCTGTTG GCTTACAAAA  | 4920 |
| GACATGGCCC ATAAGGCGCA AGGTTTTGGA CTGGACGTTT TCGCGGGCAG CCAACGTATC  | 4980 |
| TCTGCCTTAT TAAAATGTGT CCTGCTTCGG CATATGGGAG AGTTTATTGG TGTTCAGGAA  | 5040 |
| ACGCGTTATC TAATGAATGC GATGGAAAAA AACTACTCTG AGCTGGTGAA AGAGCTTCAG  | 5100 |
| CGCCAGTTAC CCATTAATAA AATCGCTGAA ACTTTGCAAC GGCTTGATATC AGAGCGGGTT | 5160 |
| TCTATTAGAG ATTTACGTCT TATTTTCGGC ACCTTAATTG ACTGGGCGCC ACGTGAAAAA  | 5220 |
| GATGTCCTGA TGTTGACAGA ATATGTCCGT ATCGCGCTTC GTCGTCATAT TCTGCGTCGT  | 5280 |
| CTTAATCCGG AAGGAAAACC GCTGCCGATT TTGCGGATCG GCGAAGGTAT TGAAAACCTC  | 5340 |
| GTGCGTGAAT CCATTCGCCA GACGGCAATG GGGACCTATA CTGCGCTGTC GTCTCGTCAT  | 5400 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| AAGACGCAGA TCCTGCAACT TATCGAGCAG GCGCTGAAGC AGTCAGCCAA ATTATTCATT  | 5460 |
| GTCACTTCTG TCGACACCCG ACGTTTCTTG CGAAAAATTA CAGAAGCCAC CTTGTTCGAC  | 5520 |
| GTACCGATTT TGTCATGGCA GGAATTAGGA GAGGAGAGCC TTATACAAGT GGTAGAAAGT  | 5580 |
| ATTGACCTTA GCGAAGAGGA GTTGGCGGAC AATGAAGAAT GAATTGATGC AACGTCTGAG  | 5640 |
| GCTGAAATAT CCGCCCCCG ATGGTTATTG TCGATGGGGC CGAATTCAGG ATGTCAGCGC   | 5700 |
| AACGTTGTTA AATGCGTGGT TGCCTGGGGT ATTTATGGGC GAGTTGTGCT GTATAAAGCC  | 5760 |
| TGGAGAAGAA CTTGCTGAAG TCGTGGGGAT TAATGGCAGC AAAGCTTTC TATCTCCTTT   | 5820 |
| TACGAGTACA ATCGGGCTTC ACTGCGGGCA GCAAGTGATG GCCTTAAGCG ACGCCATCAG  | 5880 |
| GTTCCCGTGG GCGAAGCGTT ATTAGGGCGA GTTATTGATG GCTTTGGTCG TCCCCTTGAT  | 5940 |
| GGCCGCGAAC TGCCCGACGT CTGCTGGAAA GACTATGATG CAATGCCTCC TCCCGCAATG  | 6000 |
| GTTTCGACAGC CTATCACTCA ACCATTAATG ACGGGGATTC GCGCTATTGA TAGCGTTGCG | 6060 |
| ACCTGTGGCG AAGGGCAACG AGTGGGTATT TTTTCTGCTC CTGGCGTGGG GAAAAGCACG  | 6120 |
| CTTCTGGCGA TGCTGTGTAA TGCGCCAGAC GCAGACAGCA ATGTTCTGGT GTTAATTGGT  | 6180 |
| GAACGTGGAC GAGAAGTCCG CGAATTCATC GATTTTACAC TGTCTGAAGA GACCCGAAAA  | 6240 |
| CGTTGTGTCA TTGTTGTGCG AACCTCTGAC AGACCCGCCT TAGAGCGCGT GAGGGCGCTG  | 6300 |
| TTTGTGGCCA CCACGATAGC AGAATTTTTT CGCGATAATG GAAAGCGAGT CGTCTTGCTT  | 6360 |
| GCCGACTCAC TGACGCGTTA TGCCAGGGCC GCACGGAAAT CGCTCTGGCG CCGGAGAGAC  | 6420 |
| CGCGGTTTTCT GGAGAATATC GCCAGGCGTA TTTAGTGCAT TGCCACGACT TTTAGAACGT | 6480 |
| ACGGGAATGG GAGAAAAAGG CAGTATTACC GCATTTTATA CGGTACTGGT GGAAGGCGAT  | 6540 |
| GATATGAATG AAGCCGTTGG CGGATGAAGT CCGTTCACTG CTTGATGGAC ATATTGTACT  | 6600 |
| ATCCCGACGG CTTGCAGAGA GGGGGCATT TAATGCCATT GACGTGTTGG CAACGCTCAG   | 6660 |
| CCGCGTTTTT CCAGTCGTTA CCAGCCATGA GCATCGTCAA CTGGCGGCGA TATTGCGACG  | 6720 |
| GTGCCTGGCG CTTTACCAGG AGGTTGAACT GTTAATACGC ATTGGGGAAT ACCAGCGAGG  | 6780 |
| AGTTGATACA GATACTGACA AAGCCATTGA TACCTATCCG GATATTTGCA CATTTTTCG   | 6840 |
| ACAAAGTAAG GATGAAGTAT GCGGACCCGA GCTACTTATA GAAAAATTAC ACCAAATACT  | 6900 |
| CACCGAGTGA TCATGGAAAC TTTGCTGGAG ATAATCGCGC GGCTGAAAAG CAATTACGCG  | 6960 |
| GCAAGCTTAC CGTACTTGAT CAGCAGCAAC AGGCGATTAT TACGGAACAG CAGATTTGCC  | 7020 |
| AGACGCGCGC TTTAGCAGTG TCTACCAGAC TGAAAGAATT AATGGGCTGG CAAGGTACGT  | 7080 |
| TATCTTGTC A TTTATTGTTG GATAAGAAAC AACAAATGGC CGGGTTATTC ACTCAGGCGC | 7140 |

|            |            |             |             |             |             |      |
|------------|------------|-------------|-------------|-------------|-------------|------|
| AGAGCTTTTT | GACGCAACGG | CAAGCAGTTA  | GAGAATCAGT  | ATCAGCAGCT  | TGTCTCCCGG  | 7200 |
| CGAAGCGAAT | TACAGAAGAA | TTTTAATGCG  | CTTATGAAAA  | AGAAAGAAAA  | AATTACTATG  | 7260 |
| GTATTAAGCG | ATGCGTATTA | CCAAAGTTGA  | GGGAAGTCTT  | GGGTTGCCAT  | GCCAGTCTTA  | 7320 |
| TCAGGATGAT | AACGAGGCGG | AGGCGGAACG  | TATGGACTTT  | GAACAACTCA  | TGCACCAGGC  | 7380 |
| ATTACCCATT | GGTGAGAATA | ATCCTCCTGC  | AGCATTGAAT  | AAGAACGTGG  | TTTTACGCA   | 7440 |
| ACGTTATCGT | GTTAGTGGCG | GTTATCTTGA  | CGGTGTAGAG  | TGTGAAGTAT  | GTGAATCAGG  | 7500 |
| GGGGCTAATC | CAGTTAAGAA | TCAATGTCCC  | TCATCATGAA  | ATTTACCGTT  | CGATGAAAGC  | 7560 |
| GCTAAAGCAG | TGGCTGGAGT | CTCAGTTGCT  | GCATATGGGG  | TATATAATTT  | CCCTGGAGAT  | 7620 |
| ATTCTATGTT | AAGAATAGCG | AATGAAGAGC  | GTCCGTGGGT  | GGAGATACTT  | CCAACGCAAG  | 7680 |
| GCGCTACCAT | TGGTGAGCTG | ACATTGAGTA  | TGCAACAATA  | TCCAGTACAG  | CAAGGGACAT  | 7740 |
| TATTTACCAT | AAATTATCAT | AATGAGCTGG  | GTAGGGTGTG  | GATTGCAGAA  | CAATGCTGGC  | 7800 |
| AGCGCTGGTG | TGAAGGGCTA | ATTGGCACCG  | CTAATCGATC  | GGCTATCGAT  | CCTGAATTGC  | 7860 |
| TATATGGAAT | AGCTGAATGG | GGGCTGGCGC  | CGTTATTGCA  | AGCCAGTGAT  | GCAACCCTCT  | 7920 |
| GTCAGAACGA | GCCGCCAACA | TCCTGCAGTA  | ATCTACCACA  | TCAGCTAGCG  | TTGCATATTA  | 7980 |
| AATGGACAGT | TGAAGAGCAT | GAGTTCCATA  | GCATTATTTT  | TACATGGCCA  | ACGGGTTTTT  | 8040 |
| TGCGCAATAT | AGTCGGAGAG | CTTTCTGCTG  | AGCGACAACA  | GATTTATCCT  | GCCCCTCCTG  | 8100 |
| TGGTAGTCCC | TGTATATTCA | GGCTGGTGCC  | AGCTTACATT  | AATCGAACTT  | GAGTCTATCG  | 8160 |
| AAATCGGCAT | GGGCGTTCGG | ATTCATTGCT  | TCGGCGACAT  | CAGACTCGGT  | TTTTTTGCTA  | 8220 |
| TTCAACTACC | TGGGGGAATC | TACGCAAGGG  | TGTTGCTGAC  | AGAGGATAAC  | ACGATGAAAT  | 8280 |
| TTGACGAATT | AGTCCAGGAT | ATCGAAACGC  | TACTTGCGTC  | AGGGAGCCCA  | ATGTCAAAGA  | 8340 |
| GTGACGGAAC | GTCTTCAGTC | GAAC TTGAGC | AGATAACCACA | ACAGGTGCTC  | TTTGAGGTCTG | 8400 |
| GACGTGCGAG | TCTGGAAATT | GGACAATTAC  | GACAACTTAA  | AACGGGGGAC  | GTTTTGCCTG  | 8460 |
| TAGGTGGATG | TTTTGCGCCA | GAGGTGACGA  | TAAGAGTAAA  | TGACCGTATT  | ATTGGGCAAG  | 8520 |
| GTGAGTTGAT | TGCCTGTGGC | AATGAATTTA  | TGGTGCGTAT  | TACACGTTGG  | TATCTTTGCA  | 8580 |
| AAAATACAGC | GTAAACCTGA | TAAGAAAAAT  | AATATGCGAA  | CAATATAATA  | GCGTTCCAGG  | 8640 |
| TCGTGTCATG | AGAGATACAG | TATGTCTTTA  | CCCGATTTCG  | CTTTGCAACT  | GATTGGTATA  | 8700 |
| TTGTTTCTGC | TTTCAATACT | GCCTCTCATT  | ATCGTCATGG  | GAAC TTCTTT | CCTTAAACTG  | 8760 |
| GCGGTGGTAT | TTTCGATTTT | ACGAAATGCT  | CTGGGTATTTC | AACAAGTCCC  | CCCAAATATC  | 8820 |

|       |         |         |        |        |         |        |         |        |        |        |        |       |
|-------|---------|---------|--------|--------|---------|--------|---------|--------|--------|--------|--------|-------|
| GCAC  | TGTATG  | GCCTTGC | GCT    | TGCTT  | TCC     | TTATT  | CATTA   | TGGGG  | CCGAC  | GCTAT  | TAGCT  | 8880  |
| GTAAA | AAGAGC  | GCTGGC  | CATCC  | GGTTC  | CAGGTC  | GCTGGC | GCTC    | CTTT   | CTGGAC | GTCTG  | AGTGG  | 8940  |
| GACAG | TAAAG   | CATTAG  | CGCC   | TTATC  | GACAG   | TTTTT  | TGCAAA  | AAACT  | CTGA   | AGAGA  | AAGGAA | 9000  |
| GCCA  | ATTATT  | TTCGGA  | ATTT   | GATAAA | ACGA    | ACCT   | TGGCCTG | AAGAC  | ATAAA  | AAGAA  | AGATA  | 9060  |
| AAAC  | CTGATT  | CTTTG   | CTCAT  | ATTAAT | TCCG    | GCATTT | TACGG   | TGAGT  | CAGTT  | AACGC  | CAGGCA | 9120  |
| TTTC  | GGATTG  | GATTAC  | TTAT   | TCTT   | CCC     | TTTCT  | TGGCTA  | TTGAC  | CTGCT  | TATTT  | CAAAT  | 9180  |
| ATACT | GCTGG   | CTATG   | GGGAT  | GATGAT | GGTG    | TCGCC  | GATGA   | CCATT  | TTCATT | ACCGT  | TTAAG  | 9240  |
| CTGCT | AATAT   | TTTTAC  | TGGC   | AGGCG  | GTTGG   | GATCT  | GACAC   | TGGCG  | CAATT  | GGTAC  | AGAGC  | 9300  |
| TTTT  | CATGAA  | TGATT   | CTGAA  | TTGAC  | GCAAT   | TTGTA  | ACGCA   | ACTTT  | TATGG  | ATCGT  | CCTTT  | 9360  |
| TTAC  | GCTCTAT | GCCGG   | TAGTG  | TTGGT  | TGGCAT  | CGGTAG | TGTGG   | TGTCAT | CGTA   | AGCTT  | TGTTT  | 9420  |
| AGGC  | CTTGAC  | TCAAAT  | ACAG   | GACCA  | AACGC   | TACAG  | TTCAT   | GATTAA | ATTA   | TTGGC  | CAATTG | 9480  |
| CAATA | ACCTT   | AATGG   | TCAGC  | TACCC  | CATGGC  | TTAGC  | GGTAT   | CCTGT  | TGAAT  | TATAC  | CCGGC  | 9540  |
| AGATA | AATGTT  | ACGAAT  | TGGA   | GAGCAT | TGGTT   | GAATG  | GCACA   | ACAGG  | TAAAT  | GAGTG  | GCTTA  | 9600  |
| TTGC  | ATTGGC  | TGTGG   | CTTTT  | ATTCG  | ACCAT   | TGAGC  | CTTTC   | TTTAT  | TACTT  | CCCTT  | TATTAA | 9660  |
| AAAGT | TGGCAG  | TTTAG   | GGGCC  | GCAC   | TTTTTAC | GTAAT  | TGGCGT  | GCTTAT | TGTCA  | CTTAC  | CTTTC  | 9720  |
| CGAT  | ATTACC  | AATCAT  | TTAC   | CAGCA  | GAGA    | TTATG  | ATGCA   | TATTG  | GTAAA  | GATTAC | AGTT   | 9780  |
| GGTT  | AGGGTT  | AGTCA   | CTGGA  | GAGGT  | GATTA   | TTGGT  | TTTTTC  | AATTG  | GGTTT  | TGTGC  | GGCGG  | 9840  |
| TTCC  | CTTTTG  | GGCCG   | TTGAT  | ATGGC  | GGGGT   | TTCTG  | CCTGA   | TACTTT | TACGT  | GGCGC  | GACAA  | 9900  |
| TGGG  | TACGAT  | ATTCA   | ATTCT  | ACAAT  | AGAAG   | CTGAA  | ACCTC   | ACTTTT | TGGC   | TTGCT  | TTTTCA | 9960  |
| GCCAG | TCTT    | GTGTG   | TTATT  | TTCTT  | TATAA   | GCGGC  | GGCAT   | GGAGT  | TTATA  | TTAAAC | ATTC   | 10020 |
| TGTAT | GAGTC   | ATATC   | AATAT  | TTACC  | ACCAG   | GGCGT  | ACTTT   | ATTATT | TGAC   | CAGCA  | ATTTT  | 10080 |
| TAAA  | ATATAT  | CCAGG   | CAGAG  | TGGAG  | AACGC   | TTTAT  | CAATT   | ATGTAT | CAGC   | TTCTC  | TCTTC  | 10140 |
| CTGCC | CATAAT  | ATGTAT  | TGGTA  | TTAGC  | CGATC   | TGGCT  | TTAGG   | TCTTTT | TAAAT  | CGGTC  | GGCAC  | 10200 |
| AACA  | ATTGAA  | TGTGT   | TTTTTC | TTCTC  | AATGC   | CGCTC  | AAAAG   | TATATT | TGGTT  | CTACT  | GACGY  | 10260 |
| CCTG  | ATCTCA  | TTCCCT  | TATG   | CTCTT  | CATCA   | CTATTT | TGGTT   | GAAAG  | CGATA  | AATTT  | TATAT  | 10320 |
| TTATC | TAAAA   | GACTG   | GTTTC  | CATCT  | TGATG   | AGCGA  | GAAAA   | CAGAA  | CAGCC  | TACAG  | AAAAG  | 10380 |
| AAATT | TACGTG  | ATGGC   | CGTAA  | GGAAG  | GGCAG   | GTTGT  | CAAAA   | GTATT  | GAAAT  | AACAT  | CATTA  | 10440 |
| TTTC  | CAGCTGA | TTGCG   | CTTTA  | TTTGT  | ATTTT   | CATTT  | CTTTA   | CTGAA  | AAGAT  | GATTT  | TGATA  | 10500 |
| CTGAT | TGAGT   | CAATA   | ACTTT  | CACAT  | TACAA   | TTAGT  | TAAATA  | AACCA  | TTTTTC | TTATG  | CATTA  | 10560 |

|            |            |             |            |            |             |       |
|------------|------------|-------------|------------|------------|-------------|-------|
| ACGCAATTGA | GTCATGCTTT | AATAGAGTCA  | CTGACTTCTG | CACTGCTGTT | TCTGGGCGCT  | 10620 |
| GGGGTAATAG | TTGCTACTGT | GGGTAGCGTG  | TTTCTTCAGG | TGGGGGTGGT | TATTGCCAGC  | 10680 |
| AAGGCCATTG | GTTTTAAAAG | CGAGCATATA  | AATCCGGTAA | GTAATTTTAA | GCAGATATTC  | 10740 |
| TCTTTACATA | GCGTAGTAGA | ATTATGTAAA  | TCCAGCCTAA | AAGTTATCAT | GCTATCTCTT  | 10800 |
| ATCTTTGCCT | TTTTCTTTTA | TTATTATGCC  | AGTACTTTTC | GGGCGCTACC | GTA CTGTGGG | 10860 |
| TTAGCCTGTG | GCGTGCTTGT | GTTTCTTCT   | TTAATAAAAT | GTTATGGGT  | AGGGGTGATG  | 10920 |
| GTTTTTTATA | TCGTCGTTGG | CATACTGGAC  | TATTCTTTTC | AATATTATAA | GATTAGAAAA  | 10980 |
| GCTATCTAAA | AATGAGTAAA | GATGACGTAA  | AACAGGAGCA | TAAAGATCTG | GAGGGCGACC  | 11040 |
| CTCAAATGAA | GACGCGGCGT | CGGAAATGCA  | GAGTGAAATA | CAAAGTGGGA | GTTTAGCTCA  | 11100 |
| ATCTGTTAAA | CAATCTGTTG | CGGTAGTGCG  | TAATCCAACG | CATATTGCGG | TTTGTCTTGG  | 11160 |
| CTATCATCCC | ACCGATATGC | CAATACCACG  | CGTCCTGGAA | AAAGGCAGTG | ATGCTCAAGC  | 11220 |
| TAACTATATT | GTTAACATCG | CTGAACGCAA  | CTGCATCCCC | GTTGTTGAAA | ATGTTGAGCT  | 11280 |
| GGCCCGCTCA | TTATTTTTTG | AAGTGGAAACG | CGGAGATAAA | ATTCTTGAAA | CGTTATTTGA  | 11340 |
| ACCCGTTGCA | GCCTTGTTAC | GTATGGTGAT  | GAAGATAGAT | TATGCGCATT | CTACCGAAAC  | 11400 |
| ACCATAAATG | CTTTTGGTAT | GCTTCTTCAG  | GCCACTGCGA | AGGTTAAGAG | GGTAATAGCG  | 11460 |
| TATAGAGCAG | TGCTTGACGA | TAAAGGTGAG  | AGACTGAAAA | TAATCGCTTT | TAGCCTGGCA  | 11520 |
| CAAGCACCAG | ATAGCGTATT | ATAAAATTAA  | ACAAGATAAT | GGATTGGTGC | GTCTGAATGG  | 11580 |
| ACTCGAACCA | CTCGACCCCC | ACCATGTCAA  | GGTGGTGCTC | TAACCAACTG | AGCTATGAAC  | 11640 |
| GGCAACGTTG | TAGGTGACAA | CGGGGACGAA  | TATTAGCGTC | ACAACCGCAA | TGAGGCAAGA  | 11700 |
| GGGAAATCGC | AATTTTCTTC | CTGAAATCAC  | CTGATTGCGG | TGGAAATATG | CAACATGTCTG | 11760 |
| AGAAAATAGC | CGCCATGCGA | CGGCTATCGT  | CGTATTATCG | GAGCGCGCTG | CAAAAATGATG | 11820 |
| GCGGACGGCT | GACGTTGTAG | ATAGCGCATC  | CGTAGCATCA | TTAACACCGC | CGCCGAGGTC  | 11880 |
| AGGCCGATGA | TGAACCCCAT | CCAGAAGCCT  | GCCGGTCCCA | TACGATCCAC | CACCAAATCC  | 11940 |
| GTTAACGCCA | GGATATAACC | GCTGGGTAAA  | CCTAACACCC | AGTAGGCGGT | AAAGGTGATA  | 12000 |
| AAAAAGATGG | AACGCGTATC | TTTATAACCG  | CGCAGAATAC | CGCTGCCGAT | AACCTGTATA  | 12060 |
| GAGTCGGAAA | TCTGGTAAAC | CGCAGCGAGC  | AGCATTAATT | GCGGCAAGCG | CCACGACCTC  | 12120 |
| AGGGTTGTCA | TTGTAGAGCA | AAGCAATATG  | CTTACGCAGA | GTAACGGTAA | AAATAGCGGT  | 12180 |
| AACCACAGCC | ATACAAATGC | CGACGCCTAA  | ACCGGTACGC | GCTGCGTTTG | CGCATCCAGC  | 12240 |

0094460 11600

|                                                                     |       |
|---------------------------------------------------------------------|-------|
| GTTGAGCCCT GGCCCAGACC GATAACCCAC TCGAATCGTT ACCGCCGCAG CCAGCGACAT   | 12300 |
| CGGCAGTACG AACATCAGCG AGCTAAAGTT AAGCGCAATC TGATGACCGG CGACATCCAC   | 12360 |
| AATACCTAAT GGCGAAACCA GCAGCGCAAC GACCGCAAAT AACGTCAC'TT CAAAGAACAG  | 12420 |
| CCAGCGCAAT CGGCAACCCC AGTTGAATCA GGCGCTTCAT GACGACGCTA TCGGGTTTGC   | 12480 |
| CAAAGCCTTT TTCATTACGA ATATCAGCGA TTGAACGCGC GTGTTTAAATG TAAGAAAGCA  | 12540 |
| TGGCGATAAA CATCACCCAA TAGACCGCCG CAGTCGCAAC GCCGCAGCCG ATACCGCCGA   | 12600 |
| GTTCCGGCAT ACCAAAATGG CCATAGATAA AAATATAGTT CACCGGAATA TTCACCAGCA   | 12660 |
| GGCCCCAAAA TCCCATCACC ATACCCGGTT TGGTTTTGGC CAGACCTTCG CACTGGTTTC   | 12720 |
| GCGCTACCTG AAAGAAAAGG TATCCTGCGC CCCACAGCAG CGCGCGAAGA TAACCCACGG   | 12780 |
| CTTTATCGGC CAGCGCCGGA TCAATATTAT GCATAGAGCG GATAATGTAT CCGGCATTCC   | 12840 |
| ACAGGACGAT CATCACCAGC ACGGAGACAA AGCCCGCCAG CCAGAACCCT TGTCGAACCT   | 12900 |
| GATGCGCGAT ACGCTCACGA CGGCCGGAGC CATTGAGTTG CGCAATCACA GGCGTCAAGG   | 12960 |
| CCAGCAGTAA GCCGTGACCA AACAAAATGG CGGGAAGCAG ATAGAGGTGC CGATAGCGAC   | 13020 |
| GGCAGCCATG TCCGTAGCGC TATAGCCTCC CGCCATGACG GTATCGACGA ATCCATTGCG   | 13080 |
| GTCTATACCA CTGCGCAAG GATCACCGGT ATCTGAACGC TAATAACTGA CGCGCTTCAC    | 13140 |
| TGGTATACTT CTGCACGTAT TCACCTTTTA TTTTGTGTGTT ATATGAAAGA CTA AAAAGCC | 13200 |
| GCCGAAGTGG CAGCCAAAAG AAATAGCAGG GGAAATTTCA GTCTATTGTA GCGGGGTATT   | 13260 |
| ACTATTTCTC CAGTGAAAAA ACAGTTGTTA ACGGCGCATT GCTGGCAAGC TGTTTTTCCA   | 13320 |
| CCTGCTATTG TGCTGAACAG TTCTGCTTTT ATTTATTTCA GGAGTTGAAG ATATGTTTAC   | 13380 |
| GGGGATCGTA CAGGGTACCG CGAAACTGGT ATCGATA                            | 13417 |

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: DNA sequence of VGC II cluster C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGATCCTTTT TCTTTAATGC TGCTAACGTT TCTTGCAAAA TGCGTTGATG AGATTCATCC | 60  |
| AGTACACCAC TGATAACAAA AGAGCGNCGC ATTGGCNWAM MWTKRNNMRN NSCNNNACTA | 120 |



|                                                                    |      |
|--------------------------------------------------------------------|------|
| AACCGTTCTC TATTATCGCA GAAATAATAT CATCCCCCTG AGACTGATGA GAGTGACTAA  | 180  |
| TCTGCCAGTG CAATAACCCG GGAATATCTG CAAGTAATGG TTGAACCTTG CGCCATTGCT  | 240  |
| GATCCATTTG TATATCATCA TGAATTAACA CGCTCCCCGG CCCTTCGCTG GATACTTCAG  | 300  |
| CATNSSGGTA ACCCATTTTT ATCAAAACAT CCTGCACTTC TCGTACCAAT AAGTCATCAC  | 360  |
| AGATTACACC ATCCCGATAC ATGACCCCCC ATGATTGAG AGTCGCTCTC ACCTTTTGCA   | 420  |
| TCTGTTGCTG TGACGAGCAA TAACCGGACA ACTGCAGGCT GCCATCTTCT TTCCATTGCG  | 480  |
| CCCGCACATA ATGAATATTG CTTTGTCTA ATAAAACTT AACCCGCAAA GGTAAGTCAT    | 540  |
| TTACCGTTTC AGGCTGACCA CTAATACTTA ACAGGACACC CATTCCACCG ATGAAAATCA  | 600  |
| AGAATACGCC AGCCAACCAC CAGTACCCTG ATCTGGAAAC GGGTATTTGA TAATCAGCAA  | 660  |
| GTTCAACAATC CTGTTTACCA AACGCGATAS SCACTCCCGC AACCTGCAAA ACCCCACTGG | 720  |
| ATGGTAGCGG CTTATTTGGA TTAAATCTGC GGCCATTAAC TCTAACTCTG GCTTTCCCGG  | 780  |
| CATCAACAAA TAAACTATCT GCCTGTTCTC TCAGAATAAT TTTTTCATTT ATAGCCAGCG  | 840  |
| AATACAAATA TCGCATCCCT TCTCCCCCAG TGACAGGTTA CCTTCATTCA GCCATACTTC  | 900  |
| CCGGCCTTGT AAAACGTGAC CTAAAAAAGC TATTTTCCAG GAACTCTTTG GATTAACCAT  | 960  |
| GAGATATGCC ATTATTTACT ACTGAGGCTT TAATCAAAAA AAGCCTGATT AACTATGTA   | 1020 |
| CTTGAGTCGT ATCATTGCGA AACAAATGAC CTACAACAGG AATATCGCCC AATAAAGGGA  | 1080 |
| TTTTGTTTTG CGAGTGGATT TGTTTACCTT GTTTAAACCC TCCCAGCAAT NAGACTTTGC  | 1140 |
| CCGGCCAATA ATGTGGCTTG CGAANCRATT TCAGAATTTT GCACTTCGGG CAGCGGGTCT  | 1200 |
| GTNTYGCYTT KGNSTATCAC TTTGTTGTCC ATCCTGAANT ATTAAGATTA AGCATTATTT  | 1260 |
| TTTGCGTGCC ATTGTCAATTT AACAAAGCGG GTGTAACGCG WNAACAAAGA ACCCGTAGTG | 1320 |
| ATGGATTCAA GTTTAGCCAC TTTTCTCCC TGCAGTTTGG TATAGAAAGT AATATTTTAA   | 1380 |
| TCCAGCACAG CCTGGATATT ATTTAAAGTC ACCACAGATG GCTGGGAAAG TACATAAGCC  | 1440 |
| TGAGAGCTTT TTTCCAGGGC ATTCAGACGC ACCATAAAGT TTGAGGTATC GCTGATTACC  | 1500 |
| GTTGANNAAC CACTAGCACC ACCGTCATTC AAACCTGTAT TGAACGCAAT TTTCTTGCCA  | 1560 |
| CCCAGCGACA CTGCCGTTCC CCAGTCGATG CCTAACTGGT TAATATCTCC AGCATTAACA  | 1620 |
| TCGATAATTT TCACCGAAAT CTCTATCATC TGCTGGCGTT GATCTAATTC TGTGATGAGT  | 1680 |
| TTCCGATACN NNGCCATATT GGNNNCATAA TCACGAACGA TCACTGCATT CTGGCGTNGG  | 1740 |
| GTCGGCAGCA AACATNGGCA ATGCCTGTGT AGCGGGTGAA CCATTGTTCTN TCGATGACGT | 1800 |

|            |            |             |            |             |            |      |
|------------|------------|-------------|------------|-------------|------------|------|
| CGGGACGCTG | GTTTTACTCA | TCTCACGCAA  | TACACTAACG | ACCCCTGGNN  | AACCACGACG | 1860 |
| GACTGATCGC | GATATTGGTA | CTGGGTATCC  | ATCGCAGTGG | CATACTTAAG  | CGTGTATATA | 1920 |
| CTTACACTCA | CCGCACTGTC | TTTTCGTTTG  | ATTAACGCAT | TATCCAGCAC  | TGAAGCTAAT | 1980 |
| TGACTAATAC | GAGTCAGGCA | GCTGGGAACA  | CCGCTCACCT | CCACAGCTTT  | GGTACCGGTA | 2040 |
| ATTTCTTTAA | CCTCGCATCC | CGGTGATGAA  | AGGATATTCT | GGCTGCGTAA  | GTAATGAATG | 2100 |
| AACCGTCCAG | TAGATAAAAT | ATTGAAAAGTG | ATAACCTGAT | GTTTTAATAA  | CGATGCAGGA | 2160 |
| TATACATATA | ACATGCTGCC | ATCAAACCAG  | GTAAGCAAAT | CATATTGTGC  | TGCCAGGTTA | 2220 |
| TTCAAATAT  | CGACCGGTGG | TCCAGGCGGA  | ATTTTCCAC  | TAAATGTAGC  | TGTTATCAAT | 2280 |
| GGGCTAATAG | TAATAGCCGT | ATCATAGTTC  | TCTGAGAGCA | GATGTNAAAA  | CCTCTGCTAA | 2340 |
| TGGCATTGT  | CTGGCATAAA | GGGTGAAGTC  | ATTACCTTTC | CATGATAACT  | CATCACTCTT | 2400 |
| TGCTGTATTG | AGTATAAATA | GTAAAATTAA  | GATTAAACGT | TTATTTACTA  | CCATTTTATA | 2460 |
| CCCCACCCGA | ATAAAGTTTA | TGGTGATTGC  | GTATTACATT | TTTTNAAAAT  | GCAAGTTAAA | 2520 |
| GCCAGGTGTT | TTTCTATCTC | AATAGCAATA  | AGCTCAGAGC | TACTACTTGT  | GGTATAATAA | 2580 |
| CCGTTTAACC | ATCCCCCATC | CGCTGTGAGC  | TGTATAGCAT | AATCATGGAC  | GTCCGGGTGT | 2640 |
| GCGCAARCRG | TAGTGTCAMM | TAGGCAAGAC  | AAGGCTTAGG | TAAGCTTTCC  | AGGTCATTTA | 2700 |
| AGAACAAAGA | AATAGAAAAT | GCTTCTGAGA  | AAATTTCTYC | YBHNNNNNNN  | NNNNNNNNNN | 2760 |
| NNNNNNNNCA | TCAATAGTCA | TTATCCAGGA  | TSSKMTWWYM | NYKSSSCYS   | WKATMYYSWR | 2820 |
| WWTAAATGGA | ATGCCTTTTA | AAACTGCCAG  | CATGAATCCC | TCCTCAGACA  | TAAATGGGAG | 2880 |
| TTTCTATCAA | ATTCGCTCAC | AACCACATCC  | GTAAAAAGCC | TGATTACAT   | TTATTTGAC  | 2940 |
| TATACTCTTC | TTGTACAATA | TCAGGATGCT  | GTCTACATAT | ACCTTGTCAC  | AGGCGATTCT | 3000 |
| ATCATTCGGA | TTTTCCGATA | AATTNMMCAA  | TTACATTTTC | AGCATTGACA  | TAAAACTTA  | 3060 |
| CAATTTGNAA | AATTATTTAT | TAAATAAACT  | GTTACGATGT | TTTTACATCG  | CCATCTTATT | 3120 |
| AAAAAGTAAT | TGTAGTCATC | GACTNGGTTA  | TATATGAAGA | AATTTATCTT  | CCTAATGATA | 3180 |
| ACACCATCGA | TTAATCWWCT | GATGAAACTA  | TATGTACTGC | GATAGTGATC  | AAGTGCCAAA | 3240 |
| GATTTTGCAA | CAGGCAACTG | GAGGGAAGCA  | TTATGAATTT | SSTCAATCTC  | AAGAATACSS | 3300 |
| YSYRNNNNNN | TCTTTAGTAA | TCAGGCTAAC  | TTTTTTATTT | TTATTAACAA  | CAATAATTWT | 3360 |
| TTGGCTGCTA | TCTGTGCTTA | CCGCAGCTTA  | TATATCAATG | GTTTCRGAAAC | GGCAGCATAT | 3420 |
| AATAGAGGAT | TTATCCGTTC | TATCCGAGAT  | GAATATTGTA | CTAAGCAATC  | AACGGTTTGA | 3480 |
| AGAAGCTGAA | CGTGACGCTA | AAAATTTAAT  | GTATCAATGC | TCATTAGCGA  | CTGAGATTCA | 3540 |

|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| TCATAACGAT  | ATTTTCCCTG | AGGTGAGCCG  | GCATCTATCT | GTCGGTCCTT  | CAAATTGCAC  | 3600 |
| MGCCGACGCT  | NAACGGAGAG | AAGCACCGTC  | TCTTTCTGCA | GTCCTCTGAT  | ATCGATGAAA  | 3660 |
| ATAGCTTTTCG | TCGCGATAGT | TTTATTCTTA  | ATCATAAAAA | TGAGATTTTCG | TTATTATCTA  | 3720 |
| CTGATAACCC  | TTCAGATTAT | TCAACTCTAC  | AGCCTTTAAC | GCGAAAAAGC  | TTTCCTTTAT  | 3780 |
| ACCCAACCCA  | TGCCGGGTTT | TACTGGAGTG  | AACCAGAATA | CATAAACGGC  | AAAGGATGGC  | 3840 |
| AACGCTTCCG  | TTGCGGTTGC | CGATCAGGCA  | AGGCGTATTT | TTTGAGGTGA  | CGGTTAAACT  | 3900 |
| TCCCGATCTC  | ATTACTAAGA | GCCACCTGCC  | ATTAGATGAT | AGTATTCGAG  | TATGGCTGGA  | 3960 |
| TCAAAACAAC  | CACTTATTGC | CGTTTTTCATA | CATCCCGGCA | AAAAATACGT  | ACACAGTTAG  | 4020 |
| AAAATGTAAC  | GCTGCATGAT | GGATGGCAGC  | AAATTCCCGG | ATTTCTGATA  | TTACGCACAA  | 4080 |
| CCTTGCAATG  | CCCCGGATGG | AGTCTGGTTA  | CGCTGTACCC | ATACGGTAAT  | CTACATAATC  | 4140 |
| GCATCTTAAA  | AATTATCCTT | CAACAAATCC  | CCTTTACATT | AACAGCATTG  | GTGTTGATGA  | 4200 |
| CGTCGGCTTT  | TTGCTGGTTA | CTACATCGCT  | CACTGGCCAA | ACCGTTATGG  | CGTTTTGTCTG | 4260 |
| ATGTCAATTA  | TAAAACCGCA | ACTGCACCGC  | TGAGCACACG | TTTACCAGCA  | CAACGACTGG  | 4320 |
| ATGAATTAGA  | TAGTATTGCC | GGTGCTTTTA  | ACCAACTGCT | TGATACTCTA  | CAAGTCCAAT  | 4380 |
| ACGACAATCT  | GGAAAACAAA | GTCGCAGACG  | CACCCAGGCG | CTAAATGAAG  | CAAAAAAACG  | 4440 |
| CGCTGAGCNA  | GCTAACAAAC | GTAAAAGCAT  | TCATCTTACG | GTAATAAGTC  | ATGAGTTACG  | 4500 |
| TACTCCGATG  | AATGGCGTAC | TCGGTGCAAT  | TGAATTATTA | CAAACCACCC  | CTTTAAACAT  | 4560 |
| AGAGCAACAA  | GGATTAGCTG | ATACCGCCAG  | AAATTGTACA | CTGTCTTTGT  | TAGCTATTAT  | 4620 |
| TAATAATCTG  | CTGGATTTTT | CACGCATCGA  | GTCTGGTCAT | TTACACATTAC | ATATGGAAGA  | 4680 |
| AACAGCGTTA  | CTGCCGTTAC | TGGACCAGGC  | AATGCAAACC | ATCCAGGGGC  | CAGCGCNAAA  | 4740 |
| GCAAAAAACT  | GTCATTACGT | ACTTTTGTCG  | GTCAACATGT | CCCTCTCTAT  | TTTCATACCG  | 4800 |
| ACAGTATCCG  | TTTACNNCAA | ATTTTGTTTA  | ATTTACTCGG | GAACGCGGTA  | AAATTTACCG  | 4860 |
| AAACCGGAGG  | ATACGTCTGA | CGGTCAAGCG  | TCATGAGGAA | CAATTAATAT  | TTCTGGTTAG  | 4920 |
| CGATAGCGGT  | AAAGGGATTG | AAATACAGCA  | GCAGTCTCAA | ATCTTTACTG  | CTTTTTATCA  | 4980 |
| AGCAGACACA  | AATTCGCAAG | GTACAGGAAT  | TGGACTGACT | ATTGCGTCAA  | GCCTGGCTAA  | 5040 |
| AATGATGGGC  | GGTAATCTGA | CACTAAAAAG  | TGTCCCCGGG | GTGGAACCT   | GTGTCTCGCT  | 5100 |
| AGTATTACCC  | TTACAAGAAT | ACCAGCCGCC  | TCAACCAATT | AAAGGGACGC  | TGTCAGNNNC  | 5160 |
| CGTTCTGCCT  | GCATCGGCAA | CTGGCTTGCT  | GGGGAATACG | CGGTGAACCA  | CCCCACCAGC  | 5220 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| AAAATGCGCT | TCTCAANNCN | AGAGCTTTTG | TATTTCTCCG | GAAAACTCTA | CGACCTGGCG | 5280 |
| CAACAGTTAA | TATTGTGTAC | ACCAAATATG | CCAGTAATAA | ATAATTTGTT | ACCACCCTGG | 5340 |
| CAGTTGCAGA | TTCTTTTGGT | TGATGATGCC | GATATTAATC | GGGATATCAT | CGGCAAAATG | 5400 |
| CTTGTCAGCC | TGGGCCAACA | CGTCACTATT | GCCGCCAGTA | GTAACGAGGC | TCTGACTTTA | 5460 |
| TCACAACAGC | AGCGATTCGA | TTTAGTACTG | ATTGACATTA | GAATGCCAGA | AATAGATGGT | 5520 |
| ATTGAATGTG | TACGATTATG | GCATGATGAG | CCGAATAATT | TAGATCCTGA | CTGCATGTTT | 5580 |
| GTGGCACTAT | CCGCTAGCGT | ASCVNMAGAW | RWTMWTCRTY | GTDDAAAAAA | WRDGRKDHWT | 5640 |
| CATHAYANNT | TACAAAACCA | GTGACATTGG | CTACCTTAGC | TCGCTACATC | AGTATTGCCG | 5700 |
| CAGAATACCA | ACTTTTACGA | AATATAGAGC | TACAGGAGCA | GGATCC     |            | 5746 |

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

- ```
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CCACCAGCCG	CTGGGGTACC	AGGGCCAGGC	GACGGATATT	GAAATTCACG	CCCGCGAAAT	60
TTTGAAAGTA	AAAGGGCGCA	TGAATGAACT	TATGRMKYKM	MATACGGGTC	ANTCTCTTGA	120
GCAGATTGAA	SGTGATACTG	A				141

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TGAAGCGGTA GAGTACGGTT TGGTTGACTC AATTTTGACC CATCGTAATT GATGCCCTGG	60
ACGCAA	66

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CCAACCGTTG GCGGGCTACC AGGGCCAGGC GACCGATATC GAAATTCATG CCCGTGAAAT	60
TCTGAAAGTT AAAGGGCGCA TGAATGAACT TATGGCGCTT CATACGGGTC AATCATTAGA	120
ACAGATTGAA CGTGATACCG A	141

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TGAAGCGGTG GAATACGGTC TGGTCGATTC GATTCTGACC CATCGTAATT GATGCCAGAG	60
GCGCAA	66

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GATATCGAAA TTCATGCCCG TGAAATTCTG AAAGTTAAAG GGCGCATGAA TGAACCTATG	60
GCGCTTCATA CGGGTCAATC ATTAGAACAG ATTGAACGTG ATACCGA	107

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

TGAAGCGGTG GAATACGGTC TGGTCGATTC GATTCTGACC CATCGTAATT GATGCCAGAG	60
---	----



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ala Ser Ile Ile Leu Pro Glu Tyr His Gly Ala Ala Cys Gln Ala Leu  
1 5 10 15

Asn Lys Leu Asp Asn Met Ala  
20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Arg Phe Ile Val

1

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Tyr Phe Leu Leu Ser Leu Arg Ser Phe Leu Arg His Val Met Trp Ile  
1 5 10 15

Phe Ile Ala His Cys Gln Lys Met Lys Arg Ile Lys Cys Trp His Tyr  
20 25 30

Leu Cys Ser Ile Ile Leu Met Arg Lys Lys Thr Gly Arg Gly Trp Cys  
35 40 45

Asn Leu Thr Cys Arg Ala Val Gly Ser Leu Leu Met Arg Leu Arg Leu  
50 55 60

Leu Arg Leu Asn Gly Tyr Pro His Arg Ala Val Tyr Asn Gly Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Asp Val Ser Gly

1

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Val Ser Gly Ile Thr Pro Gly Arg Thr Gly Arg Arg Leu Ile Phe

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Asn Lys Glu Leu Lys Glu Cys

1

5

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Val Arg Trp Arg Gly Val Ile Asn Gly Lys Ser Asp His Cys Ala Thr

1

5

10

15

Asp Leu

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Arg Phe Ser Glu Leu Ser Cys Arg Ile Tyr Lys Ile Phe Thr Ser Gly  
1 5 10 15  
Gln Tyr Gly Gly Leu Ser Gly Lys Asn  
20 25

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg Phe Asn Arg Asp Val Asn Pro Trp Val Ala Ile Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Leu Asp Ala Ala Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ile Gln Asn Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Arg Thr Arg Glu Thr Asn Ile Leu Asp Tyr Gly Arg Tyr Gln Arg Gln  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg Glu Gly Gly Glu Val Val Asp Glu Ile Pro Leu Ser Val Asp Val  
1 5 10 15

Ile Val Asp Arg Thr Val Ile Arg Ser Gly His Pro Asp Arg Leu Phe  
20 25 30

Leu Pro Glu Thr Pro Phe Leu Ser Arg Pro Asp Pro Glu Val Leu Gln  
35 40 45

Leu Tyr Arg Tyr Phe Trp Gln Pro Ala Arg Tyr Ala Val Pro Glu Trp  
50 55 60

Leu Asp Lys Leu Gly Phe His Leu Gln Thr Ala Gly Val Met Ala Ile  
65 70 75 80

Gly Pro Ser Trp Ile Val Phe Leu Thr Glu Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Glu Glu Ala Leu Leu Phe Gln Pro Val  
1 5

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear



(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Arg Lys Leu Thr Ile Ser Tyr Pro Leu Glu Ile Leu Leu Ser His Ser  
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Leu Tyr Leu Arg Lys Ser Asn Lys Leu Arg Glu Phe His Met Leu Leu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ala Pro Leu Thr Val Arg Leu Lys Lys Ser Ser Glu Thr Pro Ile Val  
1 5 10 15

Ile Ser Val Asn Arg Lys Leu Ser Ser Asn Lys Asn  
20 25

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Arg Ala Cys Val Lys Ile Arg Trp Lys Lys Trp Lys Trp Asn Gly Trp  
 1 5 10 15

Asn Ser Met

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn Ile Tyr Lys Thr Met Lys Ile Asn Phe Val His Trp Ser Ile Thr  
 1 5 10 15

Gln Arg Ile Ile Leu Lys Ile Val  
 20

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn Arg Phe Cys Trp Pro Gly Ser Thr Asn Ser Arg  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Thr Val Leu Cys Ala Ile Val Trp His Ala Arg Pro Arg Leu Trp Arg  
 1 5 10 15

Lys Arg Glu Arg Phe Ile Cys Val Phe Ile Leu Lys Lys Arg His  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Cys Glu Lys Leu Leu Ala Ser Gly Leu Arg  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:73:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 31 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu Ser Ser Leu Val Ser Leu Pro Ile Arg Leu Asn Phe Pro Gln His  
 1 5 10 15  
 Asp Met Pro Leu Asn Phe His Phe Leu Val Ile Ser Thr Arg Tyr  
 20 25 30

- (2) INFORMATION FOR SEQ ID NO:74:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 189 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Gly Tyr Val Met Val Lys Ile Lys Glu Val Ala Met Asn Ile Lys  
 1 5 10 15  
 Ile Asn Glu Ile Lys Met Thr Pro Pro Thr Ala Phe Thr Pro Gly Gln  
 20 25 30  
 Val Ile Glu Glu Gln Glu Val Ile Ser Pro Ser Met Leu Ala Leu Gln  
 35 40 45  
 Glu Leu Gln Glu Thr Thr Gly Ala Ala Leu Tyr Glu Thr Met Glu Glu  
 50 55 60  
 Ile Gly Met Ala Leu Ser Gly Lys Leu Arg Glu Asn Tyr Lys Phe Thr  
 65 70 75 80  
 Asp Ala Glu Lys Leu Glu Arg Arg Gln Gln Ala Leu Leu Arg Leu Ile  
 85 90 95

Lys Gln Ile Gln Glu Asp Asn Gly Ala Thr Leu Arg Pro Leu Thr Glu  
 100 105 110  
 Glu Asn Ser Asp Pro Asp Leu Gln Asn Ala Tyr Gln Ile Ile Ala Leu  
 115 120 125  
 Ala Met Ala Leu Thr Ala Gly Gly Leu Ser Lys Lys Lys Lys Arg Asp  
 130 135 140  
 Leu Gln Ser Gln Leu Asp Thr Leu Gln Arg Arg Arg Asp Gly Asn Leu  
 145 150 155 160  
 Pro Phe Leu Val Tyr Trp Asn Leu Ala Lys Trp Ile Pro Tyr Ala Val  
 165 170 175  
 Leu Ser Glu Ala Phe Tyr Ala Thr Gly Asp Arg Gln Arg  
 180 185

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asn Ala Leu Ile Ala Val Val Gln Thr Arg Gly Arg Leu Ala Gly Ser  
 1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Thr Gly Pro Tyr Phe Ala Lys Ser Ser Ser Leu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

His Met His Arg Thr Leu Gly Ala Lys Ser Phe Gly Arg Ser Ile Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:78:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

(2) INFORMATION FOR SEQ ID NO:79:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

(2) INFORMATION FOR SEQ ID NO:80:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

(2) INFORMATION FOR SEO ID NO:81:



(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Ala Leu Ala Phe Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Tyr Arg Tyr Ser Phe Phe Ile Glu Asp Val Gln Ser Val Thr Pro  
1 5 10 15

Thr Thr

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Cys Ala Val Tyr Ala Asp Thr Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Arg Arg Arg Ser Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Thr Asn Ser Arg Asn Ala Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ser Lys Asp Lys Ser Gly Phe Ile Leu Ile Pro Gly Phe Gln Tyr Leu  
1 5 10 15

Gly Lys Leu Ala Phe Trp Leu Ile Met Arg Arg Gln Asp Gly Leu Gly  
20 25 30

Ser His Tyr  
35

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Tyr Ser Ala Phe Tyr Ser Ile Ser Arg Ile Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Ala Phe Ser Asn Gln Tyr Val Leu Ala Ala Arg Thr Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 759 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Asn Tyr His Asn Gly Arg Ile Leu Leu Cys Gln Ile Leu Lys Gln Thr
 1              5              10              15

Phe Leu Asp Glu Glu Leu Leu Phe Lys Ala Leu Ala Asn Trp Lys Pro
      20              25              30

Ala Ala Phe Gln Gly Ile Pro Gln Arg Leu Phe Leu Leu Arg Asp Gly
      35              40              45

Leu Ala Met Ser Cys Ser Pro Pro Leu Ser Ser Ser Ala Glu Leu Trp
      50              55              60

Leu Arg Leu His His Arg Gln Ile Lys Phe Xaa Gly Val Ala Met Arg
      65              70              75              80

Ser Trp Leu Gly Glu Gly Val Arg Ala Gln Gln Trp Leu Ser Val Cys
      85              90              95

Ala Gly Arg Gln Asp Met Val Leu Ala Thr Val Leu Leu Ile Ala Ile
      100             105             110

Val Met Met Leu Leu Pro Leu Pro Thr Trp Met Val Asp Ile Leu Ile
      115             120             125

Thr Ile Asn Leu Met Phe Ser Val Ile Leu Leu Leu Ile Ala Ile Tyr
      130             135             140

Leu Ser Asp Pro Leu Asp Leu Ser Val Phe Pro Ser Leu Leu Leu Ile
      145             150             155             160

Thr Thr Leu Tyr Arg Leu Ser Leu Thr Ile Ser Thr Ser Arg Leu Val
      165             170             175

Leu Leu Gln His Asn Ala Gly Asn Ile Val Asp Ala Phe Gly Lys Phe
      180             185             190

Val Val Gly Gly Asn Leu Thr Val Gly Leu Val Val Phe Thr Ile Ile
      195             200             205

Thr Ile Val Gln Phe Ile Val Ile Thr Lys Gly Ile Glu Arg Val Ala
      210             215             220

Glu Val Ser Ala Arg Phe Ser Leu Asp Gly Met Pro Gly Lys Gln Met
      225             230             235             240

Ser Ile Asp Gly Asp Leu Arg Ala Gly Val Ile Asp Ala Asp His Ala
      245             250             255

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Arg Thr Leu Arg Gln His Val Gln Gln Glu Ser Arg Phe Leu Gly Ala  
260 265 270

Met Asp Gly Ala Met Lys Phe Val Lys Gly Asp Thr Ile Ala Gly Ile  
275 280 285

Ile Val Val Leu Val Asn Ile Ile Gly Gly Ile Ile Ile Ala Ile Val  
290 295 300

Gln Tyr Asp Met Ser Met Ser Glu Ala Val His Thr Tyr Ser Val Leu  
305 310 315 320

Ser Ile Gly Asp Gly Leu Cys Gly Gln Ile Pro Ser Leu Leu Ile Ser  
325 330 335

Leu Ser Ala Gly Ile Ile Val Thr Arg Val Pro Gly Glu Lys Arg Gln  
340 345 350

Asn Leu Ala Thr Glu Leu Ser Ser Gln Ile Ala Arg Gln Pro Gln Ser  
355 360 365

Leu Ile Leu Thr Ala Val Val Leu Met Leu Leu Ala Leu Ile Pro Gly  
370 375 380

Phe Pro Phe Ile Thr Leu Ala Phe Phe Ser Ala Leu Leu Ala Leu Pro  
385 390 395 400

Ile Ile Leu Ile Arg Arg Lys Lys Ser Val Val Ser Ala Asn Gly Val  
405 410 415

Glu Ala Pro Glu Lys Asp Ser Met Val Pro Gly Ala Cys Pro Leu Ile  
420 425 430

Leu Arg Leu Ser Pro Thr Leu His Ser Ala Asp Leu Ile Arg Asp Ile  
435 440 445

Asp Ala Met Arg Trp Phe Leu Phe Glu Asp Thr Gly Val Pro Leu Pro  
450 455 460

Glu Val Asn Ile Glu Val Leu Pro Glu Pro Thr Glu Lys Leu Thr Val  
465 470 475 480

Leu Leu Tyr Gln Glu Pro Val Phe Ser Leu Ser Ile Pro Ala Gln Ala  
485 490 495

Asp Tyr Leu Leu Ile Gly Ala Asp Ala Ser Val Val Gly Asp Ser Gln  
500 505 510

Thr Leu Pro Asn Gly Met Gly Gln Ile Cys Trp Leu Thr Lys Asp Met  
515 520 525

Ala His Lys Ala Gln Gly Phe Gly Leu Asp Val Phe Ala Gly Ser Gln  
530 535 540

Arg Ile Ser Ala Leu Leu Lys Cys Val Leu Leu Arg His Met Gly Glu  
545 550 555 560

Phe Ile Gly Val Gln Glu Thr Arg Tyr Leu Met Asn Ala Met Glu Lys  
565 570 575

Asn Tyr Ser Glu Leu Val Lys Glu Leu Gln Arg Gln Leu Pro Ile Asn  
580 585 590

Lys Ile Ala Glu Thr Leu Gln Arg Leu Val Ser Glu Arg Val Ser Ile  
595 600 605

Arg Asp Leu Arg Leu Ile Phe Gly Thr Leu Ile Asp Trp Ala Pro Arg  
610 615 620

Glu Lys Asp Val Leu Met Leu Thr Glu Tyr Val Arg Ile Ala Leu Arg  
625 630 635 640

Arg His Ile Leu Arg Arg Leu Asn Pro Glu Gly Lys Pro Leu Pro Ile  
645 650 655

Leu Arg Ile Gly Glu Gly Ile Glu Asn Leu Val Arg Glu Ser Ile Arg  
660 665 670

Gln Thr Ala Met Gly Thr Tyr Thr Ala Leu Ser Ser Arg His Lys Thr  
675 680 685

Gln Ile Leu Gln Leu Ile Glu Gln Ala Leu Lys Gln Ser Ala Lys Leu  
690 695 700

Phe Ile Val Thr Ser Val Asp Thr Arg Arg Phe Leu Arg Lys Ile Thr  
705 710 715 720

Glu Ala Thr Leu Phe Asp Val Pro Ile Leu Ser Trp Gln Glu Leu Gly  
725 730 735

Glu Glu Ser Leu Ile Gln Val Val Glu Ser Ile Asp Leu Ser Glu Glu  
740 745 750

Glu Leu Ala Asp Asn Glu Glu  
755

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ile Asp Ala Thr Ser Glu Ala Glu Ile Ser Ala Pro Arg Trp Leu Leu  
1 5 10 15

Ser Met Gly Pro Asn Ser Gly Cys Gln Arg Asn Val Val Lys Cys Val  
20 25 30

Val Ala Trp Gly Ile Tyr Gly Arg Val Val Leu Tyr Lys Ala Trp Arg  
 35 40 45

Arg Thr Cys  
 50

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ser Arg Gly Asp  
 1

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 257 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Trp Gln Gln Ser Phe Ala Ile Ser Phe Tyr Glu Tyr Asn Arg Ala Ser  
 1 5 10 15

Leu Arg Ala Ala Ser Asp Gly Leu Lys Arg Arg His Gln Val Pro Val  
 20 25 30

Gly Glu Ala Leu Leu Gly Arg Val Ile Asp Gly Phe Gly Arg Pro Leu  
 35 40 45

Asp Gly Arg Glu Leu Pro Asp Val Cys Trp Lys Asp Tyr Asp Ala Met  
 50 55 60

Pro Pro Pro Ala Met Val Arg Gln Pro Ile Thr Gln Pro Leu Met Thr  
 65 70 75 80

Gly Ile Arg Ala Ile Asp Ser Val Ala Thr Cys Gly Glu Gly Gln Arg  
 85 90 95

Val Gly Ile Phe Ser Ala Pro Gly Val Gly Lys Ser Thr Leu Leu Ala  
 100 105 110

Met Leu Cys Asn Ala Pro Asp Ala Asp Ser Asn Val Leu Val Leu Ile  
 115 120 125

Gly Glu Arg Gly Arg Glu Val Arg Glu Phe Ile Asp Phe Thr Leu Ser  
 130 135 140

Glu Glu Thr Arg Lys Arg Cys Val Ile Val Val Ala Thr Ser Asp Arg  
 145 150 155 160  
 Pro Ala Leu Glu Arg Val Arg Ala Leu Phe Val Ala Thr Thr Ile Ala  
 165 170 175  
 Glu Phe Phe Arg Asp Asn Gly Lys Arg Val Val Leu Leu Ala Asp Ser  
 180 185 190  
 Leu Thr Arg Tyr Ala Arg Ala Ala Arg Lys Ser Leu Trp Arg Arg Arg  
 195 200 205  
 Asp Arg Gly Phe Trp Arg Ile Ser Pro Gly Val Phe Ser Ala Leu Pro  
 210 215 220  
 Arg Leu Leu Glu Arg Thr Gly Met Gly Glu Lys Gly Ser Ile Thr Ala  
 225 230 235 240  
 Phe Tyr Thr Val Leu Val Glu Gly Asp Asp Met Asn Glu Ala Val Gly  
 245 250 255

Gly

- (2) INFORMATION FOR SEQ ID NO:93:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Ser Pro Phe Thr Ala  
 1 5

- (2) INFORMATION FOR SEQ ID NO:94:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Trp Thr Tyr Cys Thr Ile Pro Thr Ala Cys Arg Glu Gly Ala Leu Ser  
 1 5 10 15

Cys His

- (2) INFORMATION FOR SEQ ID NO:95:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Arg Val Gly Asn Ala Gln Pro Arg Phe Ser Ser Arg Tyr Gln Pro  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Ala Ser Ser Thr Gly Gly Asp Ile Ala Thr Val Pro Gly Ala Leu Pro  
 1 5 10 15

Gly Gly

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Thr Val Asn Thr His Trp Gly Ile Pro Ala Arg Ser  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Tyr Leu Ser Gly Tyr Leu His Ile Phe Ala Thr Lys  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:





(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Arg Asn Gly Lys Gln Leu Glu Asn Gln Tyr Gln Gln Leu Val Ser Arg  
1 5 10 15

Arg Ser Glu Leu Gln Lys Asn Phe Asn Ala Leu Met Lys Lys Lys Glu  
20 25 30

Lys Ile Thr Met Val Leu Ser Asp Ala Tyr Tyr Gln Ser  
35 40 45

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gly Lys Ser Trp Val Ala Met Pro Val Leu Ser Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Arg Gly Gly Gly Gly Thr Tyr Gly Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Thr Thr His Ala Pro Gly Ile Thr His Trp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Ser Ser Cys Ser Ile Glu

1

5

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Glu Arg Gly Phe His Ala Thr Leu Ser Cys

1

5

10

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Trp Arg Leu Ser

1

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Arg Cys Arg Val

1

(2) INFORMATION FOR SEO ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Ile Arg Gly Ala Asn Pro Val Lys Asn Gln Cys Pro Ser Ser  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:111:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Asn Leu Pro Phe Asp Glu Ser Ala Lys Ala Val Ala Gly Val Ser Val  
 1 5 10 15

Ala Ala Tyr Gly Val Tyr Asn Phe Pro Gly Asp Ile Leu Cys  
 20 25 30

- (2) INFORMATION FOR SEQ ID NO:112:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Arg Met Lys Ser Val Arg Gly Trp Arg Tyr Phe Gln Arg Lys Ala Leu  
 1 5 10 15

Pro Leu Val Ser  
 20

- (2) INFORMATION FOR SEQ ID NO:113:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 14 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Val Cys Asn Asn Ile Gln Tyr Ser Lys Gly His Tyr Leu Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:114:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ser Ala Gly Val Lys Gly  
20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

(2) INFORMATION FOR SEO ID NO:116:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Val Arg Thr Ser Arg Gln His Pro Ala Val Ile Tyr His Ile Ser  
20 25 30

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Arg Cys Ile Leu Asn Gly Gln Leu Lys Ser Met Ser Ser Ile Ala Leu  
1 5 10 15

Phe Leu His Gly Gln Arg Val Phe Cys Ala Ile  
20 25

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ser Glu Ser Phe Leu Leu Ser Asp Asn Arg Phe Ile Leu Pro Leu Leu  
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Ser Leu Tyr Ile Gln Ala Gly Ala Ser Leu His  
1 5 10

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ser Asn Leu Ser Leu Ser Lys Ser Ala Trp Ala Phe Gly Phe Ile Ala  
1 5 10 15

Ser Ala Thr Ser Asp Ser Val Phe Leu Leu Phe Asn Tyr Leu Gly Glu

Ser Thr Gln Gly Cys Cys  
35

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Gln Arg Ile Thr Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Asn Leu Thr Asn  
1

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ser Arg Ile Ser Lys Arg Tyr Leu Arg Gln Gly Ala Gln Cys Gln Arg  
1 5 10 15

Val Thr Glu Arg Leu Gln Ser Asn Leu Ser Arg Tyr His Asn Arg Cys  
20 25 30

Ser Leu Arg Ser Asp Val Arg Val Trp Lys Leu Asp Asn Tyr Asp Asn  
35 40 45

Leu Lys Arg Gly Thr Phe Cys Leu  
50 55

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Asp Val Leu Arg Gln Arg  
 1 5

- (2) INFORMATION FOR SEQ ID NO:125:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Met Thr Val Leu Leu Gly Lys Val Ser  
 1 5

- (2) INFORMATION FOR SEQ ID NO:126:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 32 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Leu Pro Val Ala Met Asn Leu Trp Cys Val Leu His Val Gly Ile Phe  
 1 5 10 15

Ala Lys Ile Gln Arg Lys Pro Asp Lys Lys Asn Asn Met Arg Thr Ile  
 20 25 30

- (2) INFORMATION FOR SEQ ID NO:127:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 225 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Arg Ser Arg Ser Cys His Glu Arg Tyr Ser Met Ser Leu Pro Asp Ser  
 1 5 10 15



Pro Leu Gln Leu Ile Gly Ile Leu Phe Leu Leu Ser Ile Leu Pro Leu  
20 25 30

Ile Ile Val Met Gly Thr Ser Phe Leu Lys Leu Ala Val Val Phe Ser  
35 40 45

Ile Leu Arg Asn Ala Leu Gly Ile Gln Gln Val Pro Pro Asn Ile Ala  
50 55 60

Leu Tyr Gly Leu Ala Leu Val Leu Ser Leu Phe Ile Met Gly Pro Thr  
65 70 75 80

Leu Leu Ala Val Lys Glu Arg Trp His Pro Val Gln Val Ala Gly Ala  
85 90 95

Pro Phe Trp Thr Ser Glu Trp Asp Ser Lys Ala Leu Ala Pro Tyr Arg  
100 105 110

Gln Phe Leu Gln Lys Asn Ser Glu Glu Lys Glu Ala Asn Tyr Phe Arg  
115 120 125

Asn Leu Ile Lys Arg Thr Trp Pro Glu Asp Ile Lys Arg Lys Ile Lys  
130 135 140

Pro Asp Ser Leu Leu Ile Leu Ile Pro Ala Phe Thr Val Ser Gln Leu  
145 150 155 160

Thr Gln Ala Phe Arg Ile Gly Leu Leu Ile Tyr Leu Pro Phe Leu Ala  
165 170 175

Ile Asp Leu Leu Ile Ser Asn Ile Leu Leu Ala Met Gly Met Met Met  
180 185 190

Val Ser Pro Met Thr Ile Ser Leu Pro Phe Lys Leu Leu Ile Phe Leu  
195 200 205

Leu Ala Gly Gly Trp Asp Leu Thr Leu Ala Gln Leu Val Gln Ser Phe  
210 215 220

Ser  
225

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Ile Leu Asn

1

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Arg Asn Phe Tyr Gly Ser Ser Phe Leu Arg Leu Cys Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Cys Trp Trp His Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Leu Val Ser Ser  
1

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Ala Leu Phe Arg Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Leu Lys Tyr Arg Thr Lys Arg Tyr Ser Ser  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:134:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 7 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Leu Asn Tyr Trp Gln Leu Gln  
 1 5

- (2) INFORMATION FOR SEQ ID NO:135:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 11 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Trp Ser Ala Thr His Gly Leu Ala Val Ser Cys  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:136:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ile Ile Pro Gly Arg  
 1 5

- (2) INFORMATION FOR SEQ ID NO:137:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Cys Tyr Glu Leu Glu Ser Met Val Glu Trp His Asn Arg  
1 5 10

- (2) INFORMATION FOR SEQ ID NO:138:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ser Gly Leu Leu His Trp Leu Trp Leu Leu Phe Asp His  
1 5 10

- (2) INFORMATION FOR SEQ ID NO:139:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Ala Phe Leu Tyr Tyr Phe Pro Tyr  
1 5

- (2) INFORMATION FOR SEQ ID NO:140:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO  
  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Lys Val Ala Val  
1

- (2) INFORMATION FOR SEQ ID NO:141:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Gly Pro His Phe Tyr Val Met Ala Cys Leu Cys His Leu Pro Phe Arg  
 1 5 10 15  
 Tyr Tyr Gln Ser Phe Thr Ser Arg Arg Leu  
 20 25

- (2) INFORMATION FOR SEQ ID NO:142:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Cys Ile Leu Val Lys Ile Thr Val Gly  
 1 5

- (2) INFORMATION FOR SEQ ID NO:143:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Ser Leu Glu Arg  
 1

- (2) INFORMATION FOR SEQ ID NO:144:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 39 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Leu Leu Val Phe Gln Leu Gly Phe Val Arg Arg Phe Pro Phe Gly Pro  
 1 5 10 15  
 Leu Ile Trp Arg Gly Phe Cys Leu Ile Leu Tyr Val Ala Arg Gln Trp  
 61

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30

62

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Asn Ile Ser Arg Gln Ser Gly Glu Arg Phe Ile Asn Tyr Val Ser Ala  
 1 5 10 15  
 Ser Leu Phe Leu Pro  
 20

- (2) INFORMATION FOR SEQ ID NO:149:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Tyr Val Trp Tyr  
 1

- (2) INFORMATION FOR SEQ ID NO:150:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Ile Trp Leu  
 1

- (2) INFORMATION FOR SEQ ID NO:151:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile Gly Arg His Asn Asn  
 1 5

- (2) INFORMATION FOR SEQ ID NO:152:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met Cys Phe Ser Ser Gln Cys Arg Ser Lys Val Tyr Trp Phe Tyr  
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:153:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 14 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Xaa Pro Asp Leu Ile Pro Leu Cys Ser Ser Ser Leu Phe Gly  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:154:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 225 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ile Leu Tyr Leu Ser Lys Arg Leu Val Ser Ile Cys Met Ser Glu Lys  
 1 5 10 15

Thr Glu Gln Pro Thr Glu Lys Lys Leu Arg Asp Gly Arg Lys Glu Gly  
 20 25 30

Gln Val Val Lys Ser Ile Glu Ile Thr Ser Leu Phe Gln Leu Ile Ala  
 35 40 45

Leu Tyr Leu Tyr Phe His Phe Phe Thr Glu Lys Met Ile Leu Ile Leu  
 50 55 60

Ile Glu Ser Ile Thr Phe Thr Leu Gln Leu Val Asn Lys Pro Phe Ser  
 65 70 75 80

Tyr Ala Leu Thr Gln Leu Ser His Ala Leu Ile Glu Ser Leu Thr Ser  
 85 90 95

Ala Leu Leu Phe Leu Gly Ala Gly Val Ile Val Ala Thr Val Gly Ser  
 100 105 110



Val Phe Leu Gln Val Gly Val Val Ile Ala Ser Lys Ala Ile Gly Phe  
 115 120 125

Lys Ser Glu His Ile Asn Pro Val Ser Asn Phe Lys Gln Ile Phe Ser  
 130 135 140

Leu His Ser Val Val Glu Leu Cys Lys Ser Ser Leu Lys Val Ile Met  
 145 150 155 160

Leu Ser Leu Ile Phe Ala Phe Phe Phe Tyr Tyr Tyr Ala Ser Thr Phe  
 165 170 175

Arg Ala Leu Pro Tyr Cys Gly Leu Ala Cys Gly Val Leu Val Val Ser  
 180 185 190

Ser Leu Ile Lys Trp Leu Trp Val Gly Val Met Val Phe Tyr Ile Val  
 195 200 205

Val Gly Ile Leu Asp Tyr Ser Phe Gln Tyr Tyr Lys Ile Arg Lys Ala  
 210 215 220

Ile  
 225

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Val Lys Met Thr

1

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Asn Arg Ser Ile Lys Ile Trp Arg Ala Thr Leu Lys

1

5

10

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Arg Arg Gly Val Gly Asn Ala Glu  
 1 5

(2) INFORMATION FOR SEQ ID NO:158:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Asn Thr Lys Trp Glu Phe Ser Ser Ile Cys  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:159:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Thr Ile Cys Cys Gly Ser Ala  
 1 5

(2) INFORMATION FOR SEQ ID NO:160:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Ser Asn Ala Tyr Cys Gly Leu Ser Trp Leu Ser Ser His Arg Tyr Ala  
 1 5 10 15

Asn Thr Thr Arg Pro Gly Lys Arg Gln  
 20 25

(2) INFORMATION FOR SEQ ID NO:161:  
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Thr Gln Leu His Pro Arg Cys  
 1 5

(2) INFORMATION FOR SEQ ID NO:162:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ala Gly Pro Leu Ile Ile Phe  
 1 5

(2) INFORMATION FOR SEQ ID NO:163:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser Gly Thr Arg Arg  
 1 5

(2) INFORMATION FOR SEQ ID NO:164:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Thr Arg Cys Ser Leu Val Thr Tyr Gly Asp Glu Asp Arg Leu Cys Ala  
 1 5 10 15

Phe Tyr Arg Asn Thr Ile Asn Ala Phe Gly Met Leu Leu Gln Ala Thr  
 20 25 30

Ala Lys Val Lys Arg Val Ile Ala Tyr Arg Ala Val Leu Asp Asp Lys  
 35 40 45

Gly Glu Arg Leu Lys Ile Ile Ala Phe Ser Leu Ala Gln Ala Pro Asp  
 50 55 60

Ser Val Leu  
 65

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Trp Ile Gly Ala Ser Glu Trp Thr Arg Thr Thr Arg Pro Pro Pro Cys  
 1 5 10 15

Gln Gly Gly Ala Leu Thr Asn  
 20

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Ala Met Asn Gly Asn Val Val Gly Asp Asn Gly Asp Glu Tyr  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Arg His Asn Arg Asn Glu Ala Arg Gly Lys Ser Gln Phe Ser Ser  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids

68

09714602.111600

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn His Leu Ile Ala Val Glu Ile Cys Asn Met Ser Arg Lys  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:169:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Pro Pro Cys Asp Gly Tyr Arg Arg Ile Ile Gly Ala Arg Cys Lys Met  
 1 5 10 15

Met Ala Asp Gly  
 20

(2) INFORMATION FOR SEQ ID NO:170:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Arg Ile Arg Ser Ile Ile Asn Thr Ala Ala Glu Val Arg Pro Met Met  
 1 5 10 15

Asn Pro Ile Gln Lys Pro Ala Gly Pro Ile Arg Ser Thr Thr Lys Ser  
 20 25 30

Val Asn Ala Arg Ile  
 35

(2) INFORMATION FOR SEQ ID NO:171:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Pro Leu Gly Lys Pro Asn Thr Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Ala Val Lys Val Ile Lys Lys Met Glu Arg Val Ser Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Pro Arg Arg Ile Pro Leu Pro Ile Thr Cys Ile Glu Ser Glu Ile Trp  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Thr Ala Ala Ser Ser Ile Asn Cys Gly Lys Arg His Asp Leu Arg Val  
1 5 10 15

Val Ile Val Glu Gln Ser Asn Met Leu Thr Gln Ser Asn Gly Lys Asn  
20 25 30

Ser Gly Asn His Ser His Thr Asn Ala Asp Ala  
35 40

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Thr Gly Thr Arg Cys Val Cys Ala Ser Ser Val Glu Pro Trp Pro Arg  
 1 5 10 15  
 Pro Ile Thr His Ser Asn Arg Tyr Arg Arg Ser Gln Arg His Arg Gln  
 20 25 30  
 Tyr Glu His Gln Arg Ala Lys Val Lys Arg Asn Leu Met Thr Gly Asp  
 35 40 45  
 Ile His Asn Thr  
 50

(2) INFORMATION FOR SEQ ID NO:176:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Trp Arg Asn Gln Gln Arg Asn Asp Arg Lys  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:177:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Arg His Phe Lys Glu Gln Pro Ala Gln Ser Ala Thr Pro Val Glu Ser  
 1 5 10 15

Gly Ala Ser

(2) INFORMATION FOR SEQ ID NO:178:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Arg Arg Tyr Arg Val Cys Gln Ser Leu Phe His Tyr Glu Tyr His Ala  
1 5 10 15  
Leu Asn Ala Arg Val  
20

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Cys Lys Lys Ala Trp Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Thr Ser Pro Asn Arg Pro Pro Gln Ser Gln Arg Arg Ser Arg Tyr Arg  
1 5 10 15

Arg Val Pro Ala Tyr Gln Asn Gly His Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Lys Tyr Ser Ser Pro Glu Tyr Ser Pro Ala Gly Pro Lys Ile Pro Ser  
1 5 10 15

Pro Tyr Pro Val Trp Phe Trp Pro Asp Leu Arg Thr Gly Phe Ala Leu  
20 25 30



Pro Glu Arg Lys Gly Ile Leu Arg Pro Thr Ala Ala Arg Glu Asp Asn  
 35 40 45

Pro Arg Leu Tyr Arg Pro Ala Pro Asp Gln Tyr Tyr Ala  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Cys Ile Arg His Ser Thr Gly Arg Ser Ser Pro Ala Arg Arg Gln Ser  
 1 5 10 15

Pro Pro Ala Arg Thr Leu Val Glu Pro Asp Ala Arg Tyr Ala His Asp  
 20 25 30

Gly Arg Ser His  
 35

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Val Ala Gln Ser Gln Ala Ser Arg Pro Ala Val Ser Arg Asp Gln Thr  
 1 5 10 15

Lys Trp Arg Glu Ala Asp Arg Gly Ala Asp Ser Asp Gly Ser His Val  
 20 25 30

Arg Ser Ala Ile Ala Ser Arg His Asp Gly Ile Asp Glu Ser Ile Ala  
 35 40 45

Val Tyr Thr Thr Cys Ala Arg Ile Thr Gly Ile  
 50 55

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Thr Leu Ile Thr Asp Ala Leu His Trp Tyr Thr Ser Ala Arg Ile His  
1 5 10 15  
Leu Leu Phe Cys Cys Tyr Met Lys Asp  
20 25

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Lys Ala Ala Glu Val Ala Ala Lys Arg Asn Ser Arg Gly Asn Phe Ser  
1 5 10 15  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Gly Ile Thr Ile Ser Pro Val Lys Lys Gln Leu Leu Thr Ala His  
1 5 10 15  
Cys Trp Gln Ala Val Phe Pro Pro Ala Ile Val Leu Asn Ser Ser Ala  
20 25 30  
Phe Ile Tyr Phe Arg Ser  
35

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Arg Tyr Val Tyr Gly Asp Arg Thr Gly Tyr Arg Glu Thr Gly Ile Asp  
74

009111 2094160

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

5

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

5

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

1

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

75

122

1					5					10					15				
Tyr	Ala	Val	Asn	Gly	Arg	Arg	Arg	Leu	Ser	Cys	Gln	Asn	Ile	Thr	Ala				
			20					25					30						
Gln	His	Ala	Lys	Arg	Leu	Ile	Ser	Trp	Ile	Thr	Trp	His	Glu	Gly	Ser				
			35					40					45						
Ser	Tyr	Ser	Ile	Ser	Tyr	Cys	Pro	Tyr	Val	Leu	Ser	Tyr	Gly	Met					
			50					55					60						

(2) INFORMATION FOR SEQ ID NO:192:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

(2) INFORMATION FOR SEQ ID NO:193:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

(2) INFORMATION FOR SEQ ID NO:194:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Ser Ala Val Tyr  
20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Gly Tyr Leu Asp Leu Thr Val Ile Arg Ile Gly Gln Phe Thr Thr Ala  
1 5 10 15

Asp Lys Met Phe Pro Ala Asn Gln Leu Val Val Ser Pro Gln Glu Glu  
20 25 30

Gln Ala Glu Asp  
35

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Phe Phe Lys Arg Thr Lys Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Arg Asn Ala Glu Ser Asp Gly Gly Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 127 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Leu Met Ala Lys Val Thr Ile Ala Leu Pro Thr Tyr Asp Glu Gly Ser  
 1 5 10 15  
 Asn Ala Ser Pro Ser Ser Val Ala Val Phe Ile Lys Tyr Ser Pro Gln  
 20 25 30  
 Val Asn Met Glu Ala Phe Arg Val Lys Ile Lys Asp Leu Ile Glu Met  
 35 40 45  
 Ser Ile Pro Gly Leu Gln Tyr Ser Lys Ile Ser Ile Leu Met Gln Pro  
 50 55 60  
 Ala Glu Phe Arg Met Val Ala Asp Val Pro Ala Arg Gln Thr Phe Trp  
 65 70 75 80  
 Ile Met Asp Val Ile Asn Ala Asn Lys Gly Lys Val Val Lys Trp Leu  
 85 90 95  
 Met Lys Tyr Pro Tyr Pro Leu Met Leu Ser Leu Thr Gly Leu Leu Leu  
 100 105 110  
 Gly Val Gly Ile Leu Ile Gly Tyr Phe Cys Leu Arg Arg Arg Phe  
 115 120 125

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Ala Asp Leu Ile Pro Arg Cys Cys Asn Phe Ile Val Ile Ser Gly Asn  
 1 5 10 15  
 Leu Leu Val Thr Leu Tyr Arg Asn Gly Trp Ile Ser Trp Ala Phe Ile  
 20 25 30  
 Phe Lys Leu Leu Ala Leu Trp Arg Ser Ala Arg Val Gly Ser Ser Ser  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Gln Ser Val Lys

1

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Thr Lys Arg Lys Leu Cys Tyr Ser Ser Leu Phe Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Ala Lys Thr Ala Gly Ser Ser Cys Ala Ala Tyr Ile Gly Ile Cys  
1 5 10 15

Leu Trp Ala Gly Ile Ile Gln Thr Gln Val  
20 25

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Leu Phe Tyr Ala Thr Arg Val Ser Ala Ile Ala Ser Thr Val Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Asp Leu Ala Ala Ile Trp Leu Val Gly Ala Lys Arg Trp Gln Ile Thr  
 1 5 10 15

Ser Ser Ala Ser Asp Ala Thr Asn Cys Ile Ala Asp Arg Tyr Arg His  
 20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Ser Gly Ser Ala

1

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Arg Cys Gly Phe Tyr Met Arg Tyr

1

5

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Tyr Tyr Tyr Pro Leu Arg Ser Val Tyr Phe Gly Arg Arg Leu Leu Leu

1

5

10

15

Pro Arg Leu Ser Ser Trp Ser Ile Cys Tyr Glu Phe Tyr Phe Thr Ser

20

25

30

Ser Asp Gly Asn

35



(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Ala Thr Arg Ser Lys Tyr Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Val Thr Val Asp Asn Ile Thr Ile Asn Phe Ile Cys Ala Arg Ala Thr  
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Glu Ser Phe Thr Cys Tyr Cys Glu Leu Arg Leu Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Lys Asn His Pro Arg Arg Leu Ser Leu Ser Ala  
1 5 10



Tyr Arg Thr Gly Ser Val Gly Leu Val Arg Pro Thr Val Gly Arg Gln  
 1 5 10 15  
 Cys Tyr Val Pro Ser Ser Gly Thr Pro Gly His Gly Tyr Gly Gly Arg  
 20 25 30  
 Gly Ser Ala Leu Phe Ala Tyr Ser Ser  
 35 40

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Lys Arg Gly Ile Asp Ala Arg Asn Phe Trp Gln Ala Val Tyr Val Asp  
 1 5 10 15  
 Tyr Arg Ala Trp Phe Leu Ser Arg Ser Gly  
 20 25

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Thr Phe Leu Asn Thr Ile Cys Arg  
 1 5

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Ile Phe Thr Phe Ser Ser Phe Gln Arg Val Thr Glu Met Val Thr  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Ile Leu Lys Leu Met Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:220:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Arg Pro Leu Gln His Leu Pro Leu Ala Arg Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Arg Asn Lys Arg Leu Phe Arg Leu Gln Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:222:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein.  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Leu Ser Arg Ser Tyr Arg Lys Arg Arg Gly Gln Arg Ser Met Arg Arg  
1 5 10 15

Trp Lys Lys

(2) INFORMATION FOR SEQ ID NO:223:  
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Val Val Asn Cys Ala Lys Ile Ile Asn Ser Leu Met Leu Arg Asn Trp  
 1 5 10 15

Ser Ala Asp Ser Arg Leu Cys Cys Val  
 20 25

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Asn Lys Tyr Arg Arg Ile Met Gly Gln Arg Cys Val Arg Leu Pro Lys  
 1 5 10 15

Arg Ile Val Ile Leu Ile Tyr Arg Met Arg Ile Lys Leu Ser Leu Leu  
 20 25 30

Gln Trp Arg Leu Leu Pro Ala Gly Cys Gln Lys Arg Lys Asn Ala Ile  
 35 40 45

Cys Asn Arg Asn Trp Ile Arg Tyr Ser Gly Gly Gly Met Gly Thr Cys  
 50 55 60

Arg Phe  
 65

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 178 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Phe Thr Gly Thr Trp Arg Ser Gly Tyr Arg Thr Leu Ser Ser Leu Lys  
 1 5 10 15

Arg Phe Met Gln Gln Ala Ile Asp Asn Asp Glu Met Pro Leu Ser Gln  
 20 25 30

Trp Phe Arg Arg Val Ala Asp Trp Pro Asp Arg Cys Glu Arg Val Arg  
 35 40 45

Ile Leu Leu Arg Ala Val Ala Phe Glu Leu Ser Ile Cys Ile Glu Pro  
 50 55 60

Ser Glu Gln Ser Arg Leu Ala Ala Ala Leu Val Arg Leu Arg Arg Leu  
 65 70 75 80

Leu Leu Phe Leu Gly Leu Glu Lys Glu Cys Gln Arg Glu Glu Trp Ile  
 85 90 95

Cys Gln Leu Pro Pro Asn Thr Leu Leu Pro Leu Leu Leu Asp Ile Ile  
 100 105 110

Cys Glu Arg Trp Leu Phe Ser Asp Trp Leu Leu Asp Arg Leu Thr Ala  
 115 120 125

Ile Val Ser Ser Ser Lys Met Phe Asn Arg Leu Leu Gln Gln Leu Asp  
 130 135 140

Ala Gln Phe Met Leu Ile Pro Asp Asn Cys Phe Asn Asp Glu Asp Gln  
 145 150 155 160

Arg Glu Gln Ile Leu Glu Thr Leu Arg Glu Val Lys Ile Asn Gln Val  
 165 170 175

Leu Phe

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Tyr Leu Ala Phe Asn Ile  
 1 5

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Val Asn Trp Leu Ser Gly Ser Ser  
 1 5

[illegible]

(A) LENGTH: 57 amino aci

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Phe Ile Gln Leu Ala Gly Leu Ala Glu Arg Pro Leu Ala Thr Asn Met  
20 25 30

Phe Trp Arg Gln Gly Gln Tyr Glu Thr Ile Ile Thr Val Val Phe Ser  
35 40 45

Tyr Val Arg Tyr Ser Ser Lys Pro Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Thr Lys Asn Cys Phe Leu Lys Arg Trp Leu Thr Gly Asn Pro Gln Arg  
1 5 10 15

Ser Arg Val Phe Leu Asn Asp Tyr Phe Cys Cys Ala Met Gly Leu Gln  
20 25 30

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Val Val Leu His Leu Phe Pro Ala Pro Pro Ser Ser Gly Tyr Asp Tyr  
1 5 10 15

Ile Ile Asp Lys  
20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Asn Phe Xaa Glu Ser Gln Cys Val His Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Val Arg Glu Ser Gly Arg Asn Ser Gly Ser Val Tyr Ala Arg Val Gly  
1 5 10 15

Arg Ile Trp Phe Trp Arg Arg Cys Tyr  
20 25

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Cys Cys Tyr Pro Cys Arg Pro Gly Trp Leu Ile Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:



Leu Leu Ser Thr Leu Cys Phe Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Leu Leu Phe Ile Leu Val Thr Leu Ser Ile Tyr Arg Tyr Phe Arg Leu  
1 5 10 15

Tyr Tyr Leu Leu Leu His Tyr Ile Val Cys His Ser Gln Ser Ala His  
20 25 30

His Gly Trp Tyr Cys Tyr Asn Ile Met Pro Val Ile Leu Trp Met Leu  
35 40 45

Ser Val Ser Leu Ser  
50

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Glu Glu Ile Ser Pro Leu Gly Trp Ser Tyr Leu Pro Ser Leu Leu Ser  
1 5 10 15

Cys Asn Leu Leu Ser Leu Gln Lys Val Ser Arg Gly Trp Arg Lys Leu  
20 25 30

Ala His Val Ser Arg Leu Met Gly Cys Gln Ala Asn Lys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Val Ser Met Ala Ile Cys Val Pro Glu Leu Ser Met Gln Thr Met Pro  
 1 5 10 15

Val His

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Asp Ser Met Ser Ser Arg Lys Ala Ala Phe Ser Val Arg Trp Thr Val  
 1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Asn Leu Leu Lys Ala Ile Arg Leu Pro Val Leu Leu Leu Phe Trp  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Thr Leu Ser Ala Val Ser Leu Ser Leu Ser Tyr Asn Met Ile Cys Arg  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Val Arg Leu Phe Thr Leu Ile Ala Tyr Cys Gln Ser Glu Met Val Tyr  
1 5 10 15

Val Gly Lys Phe His Arg Cys  
20

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Phe Pro Leu Ala Arg Glu Leu Leu Ser Pro Val Ser Arg Val Arg Asn  
1 5 10 15

Ala Arg Thr Trp Arg Gln Ser  
20

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Val Leu Lys Leu Pro Asp Asn Leu Ser Arg Ser Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Pro Leu Trp Phe  
1

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Cys Ser Ser Leu

1

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Phe Leu Ala Phe Leu Leu Ser Leu Ser Leu Ser Phe Gln Arg Cys  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

His Cys Gln Leu Ser Ser Phe Ala Ala Lys Ser Leu Trp Phe Pro Gln  
 1 5 10 15

Met Ala Ser Lys His Arg Lys Lys Ile Val Trp Phe Pro Ala His Val  
 20 25 30

Leu

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Ser Tyr Val Leu Ala Arg Arg Tyr Ile Leu Pro Thr  
 1 5 10 92

00911"20941260

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Phe Val Ile Leu Thr Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Asp Gly Phe Tyr Leu Arg Ile Pro Ala Ser Leu Ser Leu Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Ile Leu Arg Phe Cys Leu Asn Pro Pro Lys Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Arg Tyr Cys Tyr Ile Arg Asn Pro Tyr Leu Val Tyr Leu Phe Pro Leu  
1 5 10 15

Arg Arg Ile Ile Tyr  
20

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Ala Arg Thr Leu Val Trp Trp Val Thr Ala Arg Arg Tyr Arg Thr Gly  
1 5 10 15

Trp Gly Arg Ser Val Gly Leu Gln Lys Thr Trp Pro Ile Arg Arg Lys  
20 25 30

Val Leu Asp Trp Thr Phe Ser Arg Ala Ala Asn Val Ser Leu Pro Tyr  
35 40 45

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Asn Val Ser Cys Phe Gly Ile Trp Glu Ser Leu Leu Val Phe Arg Lys  
1 5 10 15

Arg Val Ile

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Met Arg Trp Lys Lys Thr Thr Leu Ser Trp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Lys Ser Phe Ser Ala Ser Tyr Pro Leu Ile Lys Ser Leu Lys Leu Cys  
 1 5 10 15  
 Asn Gly Leu Tyr Gln Ser Gly Phe Leu Leu Glu Ile Tyr Val Leu Phe  
 20 25 30  
 Ser Ala Pro  
 35

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Leu Thr Gly Arg His Val Lys Lys Met Ser  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Gln Asn Met Ser Val Ser Arg Phe Val Val Ile Phe Cys Val Val Leu  
 1 5 10 15  
 Ile Arg Lys Glu Asn Arg Cys Arg Phe Cys Gly Ser Ala Lys Val Leu  
 20 25 30  
 Lys Thr Ser Cys Val Asn Pro Phe Ala Arg Arg Gln Trp Gly Pro Ile  
 35 40 45  
 Leu Arg Cys Arg Leu Val Ile Arg Arg Arg Ser Cys Asn Leu Ser Ser  
 50 55 60  
 Arg Arg  
 65

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Ser Ser Gln Pro Asn Tyr Ser Leu Ser Leu Leu Ser Thr Pro Asp Val  
 1 5 10 15  
 Ser Cys Glu Lys Leu Gln Lys Pro Pro Cys Ser Thr Tyr Arg Phe Cys  
 20 25 30  
 His Gly Arg Asn  
 35

- (2) INFORMATION FOR SEQ ID NO:260:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Glu Arg Arg Ala Leu Tyr Lys Trp  
 1 5

- (2) INFORMATION FOR SEQ ID NO:261:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Lys Val Leu Thr Leu Ala Lys Arg Ser Trp Arg Thr Met Lys Asn Glu  
 1 5 10 15  
 Leu Met Gln Arg Leu Arg Leu Lys Tyr Pro Pro Pro Asp Gly Tyr Cys  
 20 25 30  
 Arg Trp Gly Arg Ile Gln Asp Val Ser Ala Thr Leu Leu Asn Ala Trp  
 35 40 45  
 Leu Pro Gly Val Phe Met Gly Glu Leu Cys Cys Ile Lys Pro Gly Glu  
 50 55 60  
 Glu Leu Ala Glu Val Val Gly Ile Asn Gly Ser Lys Ala Leu Leu Ser  
 96



65                      70                      75                      80

Pro Phe Thr Ser Thr Ile Gly Leu His Cys Gly Gln Gln Val Met Ala

                        85                      90                      95

Leu Ser Asp Ala Ile Arg Phe Pro Trp Ala Lys Arg Tyr  
100 105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Leu Val Asn Val Asp Glu Lys Ser Ala Asn Ser Ser Ile Leu His Cys  
1 5 10 15  
Leu Lys Arg Pro Glu Asn Val Val Ser Leu Leu Ser Gln Pro Leu Thr  
20 25 30  
Asp Pro Pro  
35

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Gly Arg Cys Leu Trp Pro Pro Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Gln Asn Phe Phe Ala Ile Met Glu Ser Glu Ser Ser Cys Leu Pro Thr  
1 5 10 15

His

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Arg Val Met Pro Gly Pro His Gly Asn Arg Ser Gly Ala Gly Glu Thr  
1 5 10 15  
Ala Val Ser Gly Glu Tyr Arg Gln Ala Tyr Leu Val His Cys His Asp  
20 25 30

Phe

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Asn Val Arg Glu Trp Glu Lys Lys Ala Val Leu Pro His Phe Ile Arg  
1 5 10 15

Tyr Trp Trp Lys Ala Met Ile  
20

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met Lys Pro Leu Ala Asp Glu Val Arg Ser Leu Leu Asp Gly His Ile  
1 5 10 15

Val Leu Ser Arg Arg Leu Ala Glu Arg Gly His Tyr Pro Ala Ile Asp  
20 25 30

Val Leu Ala Thr Leu Ser Arg Val Phe Pro Val Val Thr Ser His Glu  
35 40 45

His Arg Gln Leu Ala Ala Ile Leu Arg Arg Cys Leu Ala Leu Tyr Gln  
50 55 60

Glu Val Glu Leu Leu Ile Arg Ile Gly Glu Tyr Gln Arg Gly Val Asp  
65 70 75 80

Thr Asp Thr Asp Lys Ala Ile Asp Thr Tyr Pro Asp Ile Cys Thr Phe  
85 90 95

Leu Arg Gln Ser Lys Asp Glu Val Cys Gly Pro Glu Leu Leu Ile Glu  
100 105 110

Lys Leu His Gln Ile Leu Thr Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Ser Trp Lys Leu Cys Trp Arg  
1 5

- (2) INFORMATION FOR SEQ ID NO:271:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 10 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Lys Ala Ile Thr Arg Gln Ala Tyr Arg Thr  
1 5 10

- (2) INFORMATION FOR SEQ ID NO:272:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 41 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Ser Ala Ala Thr Gly Asp Tyr Tyr Gly Thr Ala Asp Leu Pro Asp Ala  
1 5 10 15

Arg Phe Ser Ser Val Tyr Gln Thr Glu Arg Ile Asn Gly Leu Ala Arg  
20 25 30

Tyr Val Ile Leu Ser Phe Ile Val Gly  
35 40

- (2) INFORMATION FOR SEQ ID NO:273:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 21 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Glu Thr Thr Asn Gly Arg Val Ile His Ser Gly Ala Glu Leu Phe Asp  
 1 5 10 15

Ala Thr Ala Ser Ser  
 20

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Arg Ile Ser Ile Ser Ser Leu Ser Pro Gly Glu Ala Asn Tyr Arg Arg  
 1 5 10 15

Ile Leu Met Arg Leu  
 20

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Lys Arg Lys Lys Lys Leu Leu Trp Tyr  
 1 5

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Ala Met Arg Ile Thr Lys Val Glu Gly Ser Leu Gly Leu Pro Cys Gln  
 1 5 10 15

Ser Tyr Gln Asp Asp Asn Glu Ala Glu Ala Glu Arg Met Asp Phe Glu  
 20 25 30

Gln Leu Met His Gln Ala Leu Pro Ile Gly Glu Asn Asn Pro Pro Ala  
 35 40 45

Ala Leu Asn Lys Asn Val Val Phe Thr Gln Arg Tyr Arg Val Ser Gly  
50 55 60

Gly Tyr Leu Asp Gly Val Glu Cys Glu Val Cys Glu Ser Gly Gly Leu  
65 70 75 80

Ile Gln Leu Arg Ile Asn Val Pro His His Glu Ile Tyr Arg Ser Met  
85 90 95

Lys Ala Leu Lys Gln Trp Leu Glu Ser Gln Leu Leu His Met Gly Tyr  
100 105 110

Ile Ile Ser Leu Glu Ile Phe Tyr Val Lys Asn Ser Glu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Arg Ala Ser Val Gly Gly Asp Thr Ser Asn Ala Arg Arg Tyr His Trp  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Ala Asp Ile Glu Tyr Ala Thr Ile Ser Ser Thr Ala Arg Asp Ile Ile  
1 5 10 15

Tyr His Lys Leu Ser  
20

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Gly Val Asp Cys Arg Thr Met Leu Ala Ala Leu Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:280:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Ser Ile Gly Tyr Arg Ser  
1 5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Ile Ala Ile Trp Asn Ser  
1 5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Met Gly Ala Gly Ala Val Ile Ala Ser Gln

1 5 10

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Cys Asn Pro Leu Ser Glu Arg Ala Ala Asn Ile Leu Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Ser Thr Thr Ser Ala Ser Val Ala Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

His Tyr Phe Tyr Met Ala Asn Gly Phe Phe Ala Gln Tyr Ser Arg Arg  
1 5 10 15

Ala Phe Cys

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:



Ala Thr Thr Asp Leu Ser Cys Pro Ser Cys Gly Ser Pro Cys Ile Phe  
 1 5 10 15

Arg Leu Val Pro Ala Tyr Ile Asn Arg Thr  
 20 25

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Val Tyr Arg Asn Arg His Gly Arg Ser Asp Ser Leu Leu Arg Arg His  
 1 5 10 15

Gln Thr Arg Phe Phe Cys Tyr Ser Thr Thr Trp Gly Asn Leu Arg Lys  
 20 25 30

Gly Val Ala Asp Arg Gly  
 35

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

His Asp Glu Ile  
 1

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Arg Ile Ser Pro Gly Tyr Arg Asn Ala Thr Cys Val Arg Glu Pro Asn  
 1 5 10 15

Val Lys Glu

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Arg Asn Val Phe Ser Arg Thr  
1 5

- (2) INFORMATION FOR SEQ ID NO:292:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 8 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Ala Asp Thr Thr Thr Gly Ala Leu  
1 5

- (2) INFORMATION FOR SEQ ID NO:293:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 14 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Gly Arg Thr Cys Glu Ser Gly Asn Trp Thr Ile Thr Thr Thr  
1 5 10

- (2) INFORMATION FOR SEQ ID NO:294:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 20 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Asn Gly Gly Arg Phe Ala Cys Arg Trp Met Phe Cys Ala Arg Gly Asp  
1 5 10 15

Asp Lys Ser Lys  
20

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Pro Tyr Tyr Trp Ala Arg

1 5

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Val Asp Cys Leu Trp Gln

1 5

(2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Ile Tyr Gly Ala Tyr Tyr Thr Leu Val Ser Leu Gln Lys Tyr Ser Val

1 5 10 15

Asn Leu Ile Arg Lys Ile Ile Cys Glu Gln Tyr Asn Ser Val Pro Gly

20 25 30

Arg Val Met Arg Asp Thr Val Cys Leu Tyr Pro Ile Arg Leu Cys Asn

35 40 45

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Leu Val Tyr Cys Phe Cys Phe Gln Tyr Cys Leu Ser Leu Ser Ser Trp  
1 5 10 15  
Glu Leu Leu Ser Leu Asn Trp Arg Trp Tyr Phe Arg Phe Tyr Glu Met  
20 25 30  
Leu Trp Val Phe Asn Lys Ser Pro Gln Ile Ser His Cys Met Ala Leu  
35 40 45  
Arg Leu Tyr Phe Pro Tyr Ser Leu Trp Gly Arg Arg Tyr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Lys Ser Ala Gly Ile Arg Phe Arg Ser Leu Ala Leu Leu Ser Gly Arg  
1 5 10 15  
Leu Ser Gly Thr Val Lys His  
20

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg Leu Ile Asp Ser Phe Cys Lys Lys Thr Leu Lys Arg Arg Lys Pro  
1 5 10 15  
Ile Ile Phe Gly Ile  
20

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Asn Glu Pro Gly Leu Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:302:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 7 amino acids  
     (B) TYPE: amino acid  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Asn Leu Ile Leu Cys Ser Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:303:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 5 amino acids  
     (B) TYPE: amino acid  
     (C) STRANDEDNESS: single  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Phe Arg His Leu Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:304:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Arg Arg His Phe Gly Leu Asp Tyr Leu Phe Ile Phe Pro Phe Trp Leu  
1 5 10 15

Leu Thr Cys Leu Phe Gln Ile Tyr Cys Trp Leu Trp Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:305:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Trp Cys Arg Arg

1

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Pro Phe His Tyr Arg Leu Ser Cys

1

5

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Tyr Phe Tyr Trp Gln Ala Val Gly Ile

1

5

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

His Trp Arg Asn Trp Tyr Arg Ala Phe His Glu

1

5

10

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Ile Asp Ala Ile Cys Asn Ala Thr Phe Met Asp Arg Pro Phe Tyr Val  
1 5 10 15  
Tyr Ala Gly Ser Val Gly Gly Ile Gly Ser Trp Cys His Arg Lys Pro  
20 25 30  
Cys Ser Gly Leu Asp Ser Asn Thr Gly Pro Asn Ala Thr Val His Asp  
35 40 45

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Ile Ile Gly Asn Cys Asn Asn Leu Asn Gly Gln Leu Pro Met Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Arg Tyr Pro Val Glu Leu Tyr Pro Ala Asp Asn Val Thr Asn Trp Arg  
1 5 10 15  
Ala Trp Leu Asn Gly Thr Thr Gly Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Val Ala Tyr Cys Ile Gly Cys Gly Phe Tyr Ser Thr Ile Glu Pro Phe  
1 5 10 15  
111

Phe Ile Thr Ser Leu Ile Lys Lys Trp Gln Phe Arg Gly Arg Thr Phe  
 20 25 30

Thr

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Trp Arg Ala Tyr Val Thr Tyr Leu Ser Asp Ile Thr Asn His Leu Pro  
 1 5 10 15

Ala Glu Asp Tyr Asp Ala Tyr Trp  
 20

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Arg Leu Gln Leu Val Arg Val Ser His Trp Arg Gly Asp Tyr Trp Phe  
 1 5 10 15

Phe Asn Trp Val Leu Cys Gly Gly Ser Leu Leu Gly Arg  
 20 25

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Tyr Gly Gly Val Ser Ala  
 1 5

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids



(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Tyr Phe Thr Trp Arg Asp Asn Gly Tyr Asp Ile Gln Phe Tyr Asn Arg  
 1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Asn Leu Thr Phe Trp Leu Ala Phe Gln Pro Val Leu Val Cys Tyr Phe  
 1 5 10 15

Leu Tyr Lys Arg Arg His Gly Val Tyr Ile Lys His Ser Val  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Val Ile Ser Ile Phe Thr Thr Arg Ala Tyr Phe Ile Ile  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 93 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Pro Ala Ile Phe Lys Ile Tyr Pro Gly Arg Val Glu Asn Ala Leu Ser  
 1 5 10 15

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Ile Met Tyr Gln Leu Leu Ser Ser Cys His Asn Met Tyr Gly Ile Ser  
20 25 30  
Arg Ser Gly Phe Arg Ser Phe Lys Ser Val Gly Thr Thr Ile Glu Cys  
35 40 45  
Val Phe Leu Leu Asn Ala Ala Gln Lys Tyr Ile Gly Ser Thr Asp Xaa  
50 55 60  
Leu Ile Ser Phe Pro Tyr Ala Leu His His Tyr Leu Val Glu Ser Asp  
65 70 75 80  
Lys Phe Tyr Ile Tyr Leu Lys Asp Trp Phe Pro Ser Val  
85 90

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Ala Arg Lys Gln Asn Ser Leu Gln Lys Arg Asn Tyr Val Met Ala Val  
1 5 10 15  
Arg Lys Gly Arg Leu Ser Lys Val Leu Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

His His Tyr Phe Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Leu Arg Phe Ile Cys Ile Phe Ile Ser Leu Leu Lys Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Leu Ser His Tyr Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Ile Asn His Phe Leu Met His  
1 5

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Leu Leu His Cys Cys Phe Trp Ala Leu Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Leu Leu Leu Trp Val Ala Cys Phe Phe Arg Trp Gly Trp Leu Leu Pro  
 1 5 10 15

Ala Arg Pro Leu Val Leu Lys Ala Ser Ile  
 20 25

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Val Ile Leu Ser Arg Tyr Ser Leu Tyr Ile Ala  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Asn Tyr Val Asn Pro Ala  
 1 5

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Lys Leu Ser Cys Tyr Leu Leu Ser Leu Pro Phe Ser Phe Ile Ile Met  
 1 5 10 15

Pro Val Leu Phe Gly Arg Tyr Arg Thr Val Gly  
 20 25

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Pro Val Ala Cys Leu Trp Phe Leu Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Asn Gly Tyr Gly  
1

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Trp Phe Phe Ile Ser Ser Leu Ala Tyr Trp Thr Ile Leu Phe Asn Ile  
1 5 10 15

Ile Arg Leu Glu Lys Leu Ser Lys Asn Glu  
20 25

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Arg Lys Thr Gly Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Arg	Ser	Gly	Gly	Arg	Pro	Ser	Asn	Glu	Asp	Ala	Ala	Ser	Glu	Met	Gln
1				5					10					15	
Ser	Glu	Ile	Gln	Ser	Gly	Ser	Leu	Ala	Gln	Ser	Val	Lys	Gln	Ser	Val
			20					25					30		
Ala	Val	Val	Arg	Asn	Pro	Thr	His	Ile	Ala	Val	Cys	Leu	Gly	Tyr	His
			35				40					45			
Pro	Thr	Asp	Met	Pro	Ile	Pro	Arg	Val	Leu	Glu	Lys	Gly	Ser	Asp	Ala
	50					55					60				
Gln	Ala	Asn	Tyr	Ile	Val	Asn	Ile	Ala	Glu	Arg	Asn	Cys	Ile	Pro	Val
65					70				75					80	
Val	Glu	Asn	Val	Glu	Leu	Ala	Arg	Ser	Leu	Phe	Phe	Glu	Val	Glu	Arg
				85					90					95	
Gly	Asp	Lys	Ile	Pro	Glu	Thr	Leu	Phe	Glu	Pro	Val	Ala	Ala	Leu	Leu
			100				105							110	
Arg	Met	Val	Met	Lys	Ile	Asp	Tyr	Ala	His	Ser	Thr	Glu	Thr	Pro	
		115				120						125			

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Met	Leu	Leu	Val	Cys	Phe	Phe	Arg	Pro	Leu	Arg	Arg	Leu	Arg	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Arg	Ile	Glu	Gln	Cys	Leu	Thr	Ile	Lys	Val	Arg	Asp
											118

009714602-11600

10

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

His His Val Lys Val Val Leu  
35

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

(2) INFORMATION FOR SEQ ID NO:339:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

(2) INFORMATION FOR SEQ ID NO:340:

- 119

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

(2) INFORMATION FOR SEO ID NO:341:

Leu Arg Trp Lys Tyr Ala Thr Cys Arg Glu Asn Ser Arg His Ala Thr  
1 5 10 15

(2) INFORMATION FOR SEO ID NO:342:

Trp Arg Thr Ala Asp Val Val Asp Ser Ala Ser Val Ala Ser Leu Thr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:343:

Thr Pro Ser Arg Ser Leu Pro Val Pro Tyr Asp Pro Pro Pro Asn Pro  
1 5 10 15  
120



Leu Thr Pro Gly Tyr Asn Arg Trp Val Asn Leu Thr Pro Ser Arg Arg  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Lys Arg Trp Asn Ala Tyr Leu Tyr Asn Arg Ala Glu Tyr Arg Cys Arg  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Ser Arg Lys Ser Gly Lys Pro Gln Arg Ala Ala Leu Ile Ala Ala Ser  
 1 5 10 15

Ala Thr Thr Ser Gly Leu Ser Leu  
 20

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Ser Lys Ala Ile Cys Leu Arg Arg Val Thr Val Lys Ile Ala Val Thr  
 1 5 10 15

Thr Ala Ile Gln Met Pro Thr Pro Lys Pro Val Arg Ala Ala Phe Ala  
 20 25 30

His Pro Ala Leu Ser Pro Gly Pro Asp Arg  
 35 40

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Pro Thr Arg Ile Val Thr Ala Ala Ala Ser Asp Ile Gly Ser Thr Asn  
1 5 10 15

Ile Ser Glu Leu Lys Leu Ser Ala Ile  
20 25

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Pro Ala Thr Ser Thr Ile Pro Asn Gly Glu Thr Ser Ser Ala Thr Thr  
1 5 10 15

Ala Asn Asn Val Thr Ser Lys Asn Ser Gln Arg Asn Arg Gln Pro Gln  
20 25 30

Leu Asn Gln Ala Leu His Asp Asp Ala Ile Gly Phe Ala Lys Ala Phe  
35 40 45

Phe Ile Thr Asn Ile Thr His  
50 55

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 151 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Thr Arg Val Phe Asn Val Arg Lys His Gly Asp Lys His His Pro Ile  
1 5 10 15

Asp Arg Arg Ser Arg Asn Ala Ala Ala Asp Thr Ala Glu Phe Arg His  
20 25 30

Thr Lys Met Ala Ile Asp Lys Asn Ile Val His Arg Asn Ile His Gln  
35 40 45

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Gln Ala Gln Lys Ser His His His Thr Arg Phe Gly Phe Gly Gln Thr  
50 55 60

Phe Ala Leu Val Ser Arg Tyr Leu Lys Glu Lys Val Ser Cys Ala Pro  
65 70 75 80

Gln Gln Arg Ala Lys Ile Thr His Gly Phe Ile Gly Gln Arg Arg Ile  
85 90 95

Asn Ile Met His Arg Ala Asp Asn Val Ser Gly Ile Pro Gln Asp Asp  
100 105 110

His His Gln His Gly Asp Lys Ala Arg Gln Pro Glu Pro Leu Ser Asn  
115 120 125

Leu Met Arg Asp Thr Leu Thr Thr Ala Gly Ala Ile Glu Leu Arg Asn  
130 135 140

His Arg Arg Gln Gly Gln Gln  
145 150

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Ala Val Thr Lys Gln Asn Gly Gly Lys Gln Ile Glu Val Pro Ile Ala  
1 5 10 15

Thr Ala Ala Met Ser Val Ala Leu  
20

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Pro Pro Ala Met Thr Val Ser Thr Asn Pro Leu Arg Ser Ile Pro Leu  
1 5 10 15

Ala Gln Gly Ser Pro Val Ser Glu Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Val Val Ile

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Lys Thr Lys Lys Pro Pro Lys Trp Gln Pro Lys Glu Ile Ala Gly Glu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Lys Asn Ser Cys  
1

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Arg Arg Ile Ala Gly Lys Leu Phe Phe His Leu Leu Leu Cys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:356:

Thr Val Leu Leu Leu Phe Ile Ser Gly Val Glu Asp Met Phe Thr Gly  
1 5 10 15

Ala Glu Pro Ser Gln Glu Gln Ile Asn Phe Phe Glu Gln Leu Leu Lys  
1 5 10 15

His Gly Met Lys Val His Arg Ile Val Phe Leu Thr Val Leu Thr Phe  
1 5 10 15  
125

Phe Leu Thr Ala Cys Asp Val Asp Leu Tyr Arg Ser Leu Pro Glu Asp  
 20 25 30

Glu Ala Asn Gln Met Leu Ala Leu Leu Met Gln His His Ile Asp Ala  
 35 40 45

Lys Lys Asn Arg Lys Arg Met Val  
 50 55

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Pro Tyr Val Ser Ser Ser Arg Gln Phe Ile Asn Ala Val Glu Ala Thr  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Arg Leu Ser Ala  
 1

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Gly Ser Leu Gln Arg Arg Ile Arg Cys Phe Arg Leu Ile Ser  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Trp Tyr His Pro Arg Lys Asn Arg Gln Lys Ile Asn Phe Leu Lys Glu  
1 5 10 15  
Gln Arg Ile Glu Gly Met Leu Ser Gln Met Glu Gly Arg Asp  
20 25 30

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Pro Leu Arg Tyr Arg Leu Met Met Arg Glu Val Thr Leu Leu Arg Ala  
1 5 10 15  
Gln Leu Pro Tyr Leu  
20

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Asn Ile His Leu Arg Ser Ile Trp Arg Pro Phe Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Lys Leu Lys Ile  
1

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(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Arg Cys Gln Ser Leu Gly Cys Asn Thr Val Arg Leu Val Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Cys Ser Leu Leu Asn Ser Glu Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Leu Thr Tyr Pro Arg Asp Lys His Ser Gly Leu Trp Thr Leu Ser Thr  
1 5 10 15

Pro Ile Lys Gly Arg Trp  
20

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Asn Thr Leu Ile Arg



1

5

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Gln Asp Cys Tyr

1

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Glu Trp Ala Ser

1

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Ser Ala Ile Phe Ala

1

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(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Asp Ala Val Phe Glu Pro Thr

1

5

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Ser Arg Gly Val Ala Thr Leu Ser Leu Phe Leu Ala Thr Cys Ser Leu  
1 5 10 15  
Arg Cys Thr Gly Met Ala Gly  
20

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Ala Gly Leu Ser Ser Ser Asn Cys Trp Arg Tyr Gly Asp Arg Pro Glu  
1 5 10 15  
Leu Asp Arg Leu Leu Asp Arg Ala Leu Asn Arg Leu Arg Gly Ser Ser  
20 25 30  
Val Ile Pro Ala Cys Leu Asn Asp Arg Gln Lys Arg Gln Val Arg Leu  
35 40 45  
Ala Pro Arg Ile Ser Ala Phe Ala Phe Gly Leu Gly Leu Phe Lys Leu  
50 55 60  
Arg Cys Ser Asp Tyr Phe Met Leu Pro Glu Tyr Arg Gln Leu Leu Leu  
65 70 75 80  
Gln Trp Phe Ser Glu Asp Glu Ile Trp Gln Leu Tyr Gly Trp Leu Gly  
85 90 95  
Gln Arg Asp Gly Lys Leu Leu Pro Pro Gln Val Met Gln Gln Thr Ala  
100 105 110  
Leu Gln Ile Gly Thr Ala Ile Leu Asn Arg Glu Ala His Asp Asp Ala  
115 120 125  
Gly Phe Thr Cys Ala Ile Ser Ile Ile Thr Pro Ser Ala Ala Tyr Thr  
130 135 140  
Leu Ala Glu Asp Phe Ser Tyr Arg Asp Tyr Leu His Gly Ala Phe Ala  
130

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145                      150                      155                      160

Met Ser Phe Thr Ser Leu Pro Leu Thr Glu Ile Asn His Lys Leu Pro  
                                  165                                   170                                   175

Ala Arg Asn Ile Ile Glu Ser Gln Trp Ile Thr Leu Gln Leu Thr Leu  
                                  180                                   185                                   190

Phe Ala Gln Glu Gln Gln Ala Lys Arg Val Ser His Ala Ile Val Ser  
                                  195                                   200                                   205

Ser Ala Tyr Arg Lys Ala Glu Lys Ile Ile Arg Asp Ala Tyr Arg Tyr  
                                  210                                   215                                   220

Gln Arg Glu Gln Lys Val Glu Gln Gln Gln Glu Leu Ala Cys Leu Arg  
                                  225                                   230                                   235                                   240

Lys Asn Thr Leu Glu Lys Met Glu Val Glu Trp Leu Glu Gln His Val  
                                  245                                   250                                   255

Lys His Leu Gln Asp Asp Glu Asn Gln Phe Arg Ser Leu Val Asp His  
                                  260                                   265                                   270

Ala Ala His His Ile Lys Asn Ser Ile Glu Gln Val Leu Leu Ala Trp  
                                  275                                   280                                   285

Phe Asp Gln Gln Ser Val Asp Ser Val Met Cys His Arg Leu Ala Arg  
                                  290                                   295                                   300

Gln Ala Thr Ala Met Ala Glu Glu Gly Ala Leu Tyr Leu Arg Ile His  
                                  305                                   310                                   315                                   320

Pro Glu Lys Glu Ala Leu Met Arg Glu Thr Phe Gly Lys Arg Phe Thr  
                                  325                                   330                                   335

Leu Ile Ile Glu Pro Gly Phe Ser Pro Asp Gln Ala Glu Leu Ser Ser  
                                  340                                   345                                   350

Thr Arg Tyr Ala Val Glu Phe Ser Leu Ser Arg His Phe Asn Ala Leu  
                                  355                                   360                                   365

Leu Lys Trp Leu Arg Asn Gly Glu Asp Lys Arg Gly Ser Asp Glu Tyr  
                                  370                                   375                                   380

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Asp Lys Asn Asp Ala Pro Tyr Ser Ile Tyr Pro Trp Pro Gly Tyr Arg  
   1                                    5                                    10                                    15

Gly Thr Arg Gly Tyr Phe Ala Phe Asn Val Ser Ser Pro Gly Val Thr  
 20 25 30

Gly Asn Asp Gly Gly Ser Ala Leu  
 35 40

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Asp Asp Gly Arg Asn Arg Asn Gly Ala Glu Trp  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Thr Ala Arg Lys Leu  
 1 5

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Glu Thr Gly Ala Gln Thr Ala Gly Phe Ala Ala Phe Asp Lys Thr Asn  
 1 5 10 15

Thr Gly Gly

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Trp Gly Asn Val Ala Ser Ala Tyr Arg Arg Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Phe Thr Glu Cys Val Ser Asn Tyr Arg Ser Cys Asn Gly Ala Tyr Cys  
1 5 10 15

Arg Arg Val Val Lys Lys Glu Lys Thr Arg Phe Ala Ile Ala Thr Gly  
20 25 30

Tyr Val Thr Ala Glu Glu Gly Trp Glu Leu Ala Val Phe Ser Leu Leu  
35 40 45

Glu Leu Gly Glu Val Asp Thr Val Arg Cys Pro Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Ser Val Leu Cys Asn Arg Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Thr Thr Met Lys Cys Pro Tyr Arg Ser Gly Ser Asp Ala Trp Gln Thr  
133

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1 5 10 15

Gly Arg Ile Ala Val Asn Gly Ser Val Phe Cys  
20 25

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Pro Leu Asn Leu Ala Tyr Ala Ser Asn Pro Arg Ser Lys Val Val Trp  
1 5 10 15

Pro Gln His

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Tyr Val Cys Val Val Cys Cys Tyr Ser Leu Ala Leu Lys Lys Ser Ala  
1 5 10 15

Ser Val Arg Ser Gly Phe Ala Ser Cys Arg Leu Ile His Tyr Cys Arg  
20 25 30

Tyr Tyr Ser Ile Leu Phe Val Ser Ala Gly Phe Ser Val Ile Gly Cys  
35 40 45

Leu Ile Asp Leu Pro Leu  
50

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Phe Leu His Arg Arg Cys Ser Ile Gly Tyr Ser Asn Asn Leu Met Arg  
1 5 10 15

Ser Leu Cys

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Tyr Pro Ile Thr Val Leu Thr Thr Lys Ile Asn Val Asn Lys Phe Ser  
1 5 10 15  
Lys Arg Phe Val Lys  
20

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Ile Arg Phe Tyr Ser Asp Thr Trp Leu Ser Ile Phe Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Ile Gly Phe Leu Ala His His Glu Ala Ser Gly Trp Ile Gly Ile Ser  
1 5 10 15  
Leu Leu Asn Val Ile Phe Ser Phe Leu Phe Asn  
20 25

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear





35

40

45

Arg Asn Ala Phe Met Val Arg  
50 55

## (2) INFORMATION FOR SEQ ID NO:394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Gly Ser Gln Gly Ala Thr Val Ala Gln Cys Met Arg Gly Ser Ala Gly  
1 5 10 15

Tyr Gly Ser Gly Asp Gly Val Ile Asn Arg Tyr Cys Asp Asp Ala Val  
20 25 30

Thr Leu Ala Asp Leu Asp Gly  
35

## (2) INFORMATION FOR SEQ ID NO:395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Tyr Pro Asp Tyr Tyr Gln Pro Tyr Val Phe Ser Asp Pro Ala Leu Asn  
1 5 10 15

Cys Tyr Leu Ser  
20

## (2) INFORMATION FOR SEQ ID NO:396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Pro Ser Arg Phe Ile Gly Ile Ser Val Phe Ile Thr Tyr Tyr Tyr Ile  
1 5 10 15

Ile Ser Phe Val Thr His Asn Gln His Ile Thr Ala Gly Thr Val Thr  
137

0094460

Thr

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Tyr Cys Gly Cys Phe Arg

1

5

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Val Cys Arg Arg Arg Lys Ser His Arg Trp Val Gly Arg Ile Tyr His

1

5

10

15

His Tyr Tyr Arg Ala Ile Tyr Cys His Tyr Lys Arg Tyr Arg Glu Gly

20

25

30

Gly Gly Ser

35

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Arg Thr Phe Leu Ala

1

5

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Trp Asp Ala Arg Gln Thr Asn Glu Tyr Arg Trp Arg Phe Ala Cys Arg  
1 5 10 15  
Ser Tyr Arg Cys Arg Pro Cys Pro Tyr Ile Lys Thr Ala Cys Pro Ala  
20 25 30  
Gly Lys Pro Leu Ser Arg Cys Asp Gly Arg Cys Asp Glu Ile Cys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Arg Arg Tyr Asp Cys Arg Tyr Tyr Cys Cys Ser Gly Glu His Tyr Arg  
1 5 10 15  
Arg Tyr His Tyr Arg Tyr Arg Thr Ile  
20 25

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Tyr Val Asp Glu  
1

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Gly Cys Ser His Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:404:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Arg Thr Val Asn Arg Arg Trp Phe Met Trp Ala Asn Ser Ile Ala Ala  
1 5 10 15

Asp Phe Pro

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Arg Gly Asn Tyr Cys His Pro Cys Pro Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Glu Thr Pro Glu Pro Gly Asp Arg Val Glu Phe Ser Asn Cys Gln Thr  
1 5 10 15

Thr Ser Val Ala His Ile Asn Arg Cys Gly Phe Asn Ala Pro Arg Phe  
20 25 30

Asn Ser Trp Leu Ser Phe Tyr His Ser Arg Phe Leu Phe Ser Val Val  
35 40 45

Ser Ile Ala Asn Tyr Pro His Ser Pro Gln Lys Val Cys Gly Phe Arg  
50 55 60

Lys Trp Arg Arg Ser Thr Gly Lys Arg

65

70

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Tyr Gly Ser Arg Arg Met Ser Ser Asn Leu Thr Ser  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Pro Asp Val Thr Phe Cys Arg Pro Asp Ser  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Arg His Glu Met Val Phe Ile  
 1 5

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Gly Tyr Arg Arg Pro Ser Pro  
 1 5

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

(2) INFORMATION FOR SEQ ID NO:412:

(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

(2) INFORMATION FOR SEO ID NO:413:

(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Arg His Gly Pro  
20

(i) SEOUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Gly Ala Arg Phe Trp Thr Gly Arg Phe Arg Gly Gln Pro Thr Tyr Leu  
 1 5 10 15

Cys Leu Ile Lys Met Cys Pro Ala Ser Ala Tyr Gly Arg Val Tyr Trp  
 20 25 30

Cys Ser Gly Asn Ala Leu Ser Asn Glu Cys Asp Gly Lys Lys Leu Leu  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Ala Gly Glu Arg Ala Ser Ala Pro Val Thr His  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Asn Phe Ala Thr Ala Cys Ile Arg Ala Gly Phe Tyr  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Arg Phe Thr Ser Tyr Phe Arg His Leu Asn  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Leu Gly Ala Thr

1

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Lys Arg Cys Pro Asp Val Asp Arg Ile Cys Pro Tyr Arg Ala Ser Ser

1

5

10

15

Ser Tyr Ser Ala Ser Ser

20

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Ser Gly Arg Lys Thr Ala Ala Asp Phe Ala Asp Arg Arg Arg Tyr

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Lys Pro Arg Ala

1

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Ile His Ser Pro Asp Gly Asn Gly Asp Leu Tyr Cys Ala Val Val Ser  
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Asp Ala Asp Pro Ala Thr Tyr Arg Ala Gly Ala Glu Ala Val Ser Gln  
1 5 10 15

Ile Ile His Cys His Phe Cys Arg His Pro Thr Phe Leu Ala Lys Asn  
20 25 30

Tyr Arg Ser His Leu Val Arg Arg Thr Asp Phe Val Met Ala Gly Ile  
35 40 45

Arg Arg Gly Glu Pro Tyr Thr Ser Gly Arg Lys Tyr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Arg Arg Gly Val Gly Gly Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Asn Ile Arg Pro Pro Met Val Ile Val Asp Gly Ala Glu Phe Arg Met  
1 5 10 15  
Ser Ala Gln Arg Cys  
20

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Met Arg Gly Cys Leu Gly Tyr Leu Trp Ala Ser Cys Ala Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

Ser Leu Glu Lys Asn Leu Leu Lys Ser Trp Gly Leu Met Ala Ala Lys  
1 5 10 15

Leu Cys Tyr Leu Leu Arg Val Gln Ser Gly Phe Thr Ala Gly Ser  
20 25 30

Lys

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Ala Thr Pro Ser Gly Ser Arg Gly Arg Ser Val Ile Arg Ala Ser Tyr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Trp Leu Trp Ser Ser Pro  
 1 5

- (2) INFORMATION FOR SEQ ID NO:430:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Trp Pro Arg Thr Ala Arg Arg Leu Leu Glu Arg Leu  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:431:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Cys Asn Ala Ser Ser Arg Asn Gly Ser Thr Ala Tyr His Ser Thr Ile  
 1 5 10 15

Asn Asp Gly Asp Ser Arg Tyr  
 20

- (2) INFORMATION FOR SEQ ID NO:432:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Arg Cys Asp Leu Trp Arg Arg Ala Thr Ser Gly Tyr Phe Phe Cys Ser  
 1 5 10 15

Trp Arg Gly Glu Lys His Ala Ser Gly Asp Ala Val  
20 25

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Cys Ala Arg Arg Arg Gln Gln Cys Ser Gly Val Asn Trp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Thr Trp Thr Arg Ser Pro Arg Ile His Arg Phe Tyr Thr Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Arg Asp Pro Lys Thr Leu Cys His Cys Cys Arg Asn Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Gln Thr Arg Leu Arg Ala Arg Glu Gly Ala Val Cys Gly His His Asp  
 1 5 10 15

Ser Arg Ile Phe Ser Arg  
 20

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Trp Lys Ala Ser Arg Leu Ala Cys Arg Leu Thr Asp Ala Leu Cys Gln  
 1 5 10 15

Gly Arg Thr Glu Ile Ala Leu Ala Pro Glu Arg Pro Arg Phe Leu Glu  
 20 25 30

Asn Ile Ala Arg Arg Ile  
 35

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Cys Ile Ala Thr Thr Phe Arg Thr Tyr Gly Asn Gly Arg Lys Arg Gln  
 1 5 10 15

Tyr Tyr Arg Ile Leu Tyr Gly Thr Gly Gly Arg Arg  
 20 25

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Ser Arg Trp Arg Met Lys Ser Val His Cys Leu Met Asp Ile Leu Tyr  
 1 5 10 15

Tyr Pro Asp Gly Leu Gln Arg Gly Gly Ile Ile Leu Pro Leu Thr Cys  
                   20                  25                  30  
 Trp Gln Arg Ser Ala Ala Phe Phe Gln Ser Leu Pro Ala Met Ser Ile  
                   35                  40                  45  
 Val Asn Trp Arg Arg Tyr Cys Asp Gly Ala Trp Arg Phe Thr Arg Arg  
                   50                  55                  60  
 Leu Asn Cys  
                   65

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Tyr Ala Leu Gly Asn Thr Ser Glu Glu Leu Ile Gln Ile Leu Thr Lys  
   1                  5                  10                  15  
 Pro Leu Ile Pro Ile Arg Ile Phe Ala His Phe Cys Asp Lys Val Arg  
                   20                  25                  30  
 Met Lys Tyr Ala Asp Pro Ser Tyr Leu  
                   35                  40

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Lys Asn Tyr Thr Lys Tyr Ser Pro Ser Asp His Gly Asn Phe Ala Gly  
   1                  5                  10                  15  
 Asp Asn Arg Ala Ala Glu Lys Gln Leu Arg Gly Lys Leu Thr Val Leu  
                   20                  25                  30  
 Asp Gln Gln Gln Gln Ala Ile Ile Thr Glu Gln Gln Ile Cys Gln Thr  
                   35                  40                  45  
 Arg Ala Leu Ala Val Ser Thr Arg Leu Lys Glu Leu Met Gly Trp Gln  
                   50                  55                  60  
 Gly Thr Leu Ser Cys His Leu Leu Leu Asp Lys Lys Gln Gln Met Ala  
   65                  70                  75                  80



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Ser Val Lys Tyr Val Asn Gln Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Glu Ser Met Ser Leu Ile Met Lys Phe Thr Val Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Ser Ser Gly Trp Ser Leu Ser Cys Cys Ile Trp Gly Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 328 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Phe Pro Trp Arg Tyr Ser Met Leu Arg Ile Ala Asn Glu Glu Arg Pro  
1 5 10 15

Trp Val Glu Ile Leu Pro Thr Gln Gly Ala Thr Ile Gly Glu Leu Thr  
20 25 30

Leu Ser Met Gln Gln Tyr Pro Val Gln Gln Gly Thr Leu Phe Thr Ile  
35 40 45

Asn Tyr His Asn Glu Leu Gly Arg Val Trp Ile Ala Glu Gln Cys Trp  
50 55 60

Gln Arg Trp Cys Glu Gly Leu Ile Gly Thr Ala Asn Arg Ser Ala Ile  
152

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65		70		75		80									
Asp	Pro	Glu	Leu	Leu	Tyr	Gly	Ile	Ala	Glu	Trp	Gly	Leu	Ala	Pro	Leu
			85						90					95	
Leu	Gln	Ala	Ser	Asp	Ala	Thr	Leu	Cys	Gln	Asn	Glu	Pro	Pro	Thr	Ser
			100					105					110		
Cys	Ser	Asn	Leu	Pro	His	Gln	Leu	Ala	Leu	His	Ile	Lys	Trp	Thr	Val
		115					120					125			
Glu	Glu	His	Glu	Phe	His	Ser	Ile	Ile	Phe	Thr	Trp	Pro	Thr	Gly	Phe
	130					135					140				
Leu	Arg	Asn	Ile	Val	Gly	Glu	Leu	Ser	Ala	Glu	Arg	Gln	Gln	Ile	Tyr
145				150						155					160
Pro	Ala	Pro	Pro	Val	Val	Val	Pro	Val	Tyr	Ser	Gly	Trp	Cys	Gln	Leu
				165					170					175	
Thr	Leu	Ile	Glu	Leu	Glu	Ser	Ile	Glu	Ile	Gly	Met	Gly	Val	Arg	Ile
			180					185					190		
His	Cys	Phe	Gly	Asp	Ile	Arg	Leu	Gly	Phe	Phe	Ala	Ile	Gln	Leu	Pro
		195					200					205			
Gly	Gly	Ile	Tyr	Ala	Arg	Val	Leu	Leu	Thr	Glu	Asp	Asn	Thr	Met	Lys
	210					215					220				
Phe	Asp	Glu	Leu	Val	Gln	Asp	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Gly	Ser
225				230						235					240
Pro	Met	Ser	Lys	Ser	Asp	Gly	Thr	Ser	Ser	Val	Glu	Leu	Glu	Gln	Ile
			245					250						255	
Pro	Gln	Gln	Val	Leu	Phe	Glu	Val	Gly	Arg	Ala	Ser	Leu	Glu	Ile	Gly
			260					265					270		
Gln	Leu	Arg	Gln	Leu	Lys	Thr	Gly	Asp	Val	Leu	Pro	Val	Gly	Gly	Cys
	275						280					285			
Phe	Ala	Pro	Glu	Val	Thr	Ile	Arg	Val	Asn	Asp	Arg	Ile	Ile	Gly	Gln
	290					295					300				
Gly	Glu	Leu	Ile	Ala	Cys	Gly	Asn	Glu	Phe	Met	Val	Arg	Ile	Thr	Arg
305				310						315					320
Trp	Tyr	Leu	Cys	Lys	Asn	Thr	Ala								
			325												

- (2) INFORMATION FOR SEQ ID NO:448:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Tyr Ala Asn Asn Ile Ile Ala Phe Gln Val Val Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Glu Ile Gln Tyr Val Phe Thr Arg Phe Ala Phe Ala Thr Asp Trp Tyr  
1 5 10 15

Ile Val Ser Ala Phe Asn Thr Ala Ser His Tyr Arg His Gly Asn Phe  
20 25 30

Phe Pro

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Thr Gly Gly Gly Ile Phe Asp Phe Thr Lys Cys Ser Gly Tyr Ser Thr  
1 5 10 15

Ser Pro Pro Lys Tyr Arg Thr Val Trp Pro Cys Ala Cys Thr Phe Leu  
20 25 30

Ile His Tyr Gly Ala Asp Ala Ile Ser Cys Lys Arg Ala Leu Ala Ser  
35 40 45

Gly Ser Gly Arg Trp Arg Ser Phe Leu Asp Val  
50 55

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Ser Ile Ser Ala Leu Ser Thr Val Phe Ala Lys Lys Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Arg Glu Gly Ser Gln Leu Phe Ser Glu Phe Asp Lys Thr Asn Leu Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Arg His Lys Lys Lys Asp Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Phe Phe Ala His Ile Asn Ser Gly Ile Tyr Gly Glu Ser Val Asn Ala  
1 5 10 15

Gly Ile Ser Asp Trp Ile Thr Tyr Leu Ser Ser Leu Ser Gly Tyr  
20 25 30

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Pro Ala Tyr Phe Lys Tyr Thr Ala Gly Tyr Gly Asp Asp Asp Gly Val  
1 5 10 15  
Ala Asp Asp His Phe Ile Thr Val  
20

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Ala Ala Asn Ile Phe Thr Gly Arg Arg Leu Gly Ser Asp Thr Gly Ala  
1 5 10 15  
Ile Gly Thr Glu Leu Phe Met Asn Asp Ser Glu Leu Thr Gln Phe Val  
20 25 30  
Thr Gln Leu Leu Trp Ile Val Leu Phe Thr Ser Met Pro Val Val Leu  
35 40 45  
Val Ala Ser Val Val Gly Val Ile Val Ser Leu Val Gln Ala Leu Thr  
50 55 60  
Gln Ile Gln Asp Gln Thr Leu Gln Phe Met Ile Lys Leu Leu Ala Ile  
65 70 75 80  
Ala Ile Thr Leu Met Val Ser Tyr Pro Trp Leu Ser Gly Ile Leu Leu  
85 90 95  
Asn Tyr Thr Arg Gln Ile Met Leu Arg Ile Gly Glu His Gly  
100 105 110

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Ala Gln Gln Val Asn Glu Trp Leu Ile Ala Leu Ala Val Ala Phe  
1 5 10 15

Ile Arg Pro Leu Ser Leu Ser Leu Leu Leu Pro Leu Leu Lys Ser Gly  
                   20                                  25                                  30  
 Ser Leu Gly Ala Ala Leu Leu Arg Asn Gly Val Leu Met Ser Leu Thr  
                   35                                  40                                  45  
 Phe Pro Ile Leu Pro Ile Ile Tyr Gln Gln Lys Ile Met Met His Ile  
                   50                                  55                                  60  
 Gly Lys Asp Tyr Ser Trp Leu Gly Leu Val Thr Gly Glu Val Ile Ile  
                   65                                  70                                  75                                  80  
 Gly Phe Ser Ile Gly Phe Cys Ala Ala Val Pro Phe Trp Ala Val Asp  
                                   85                                  90                                  95  
 Met Ala Gly Phe Leu Leu Asp Thr Leu Arg Gly Ala Thr Met Gly Thr  
                   100                                  105                                  110  
 Ile Phe Asn Ser Thr Ile Glu Ala Glu Thr Ser Leu Phe Gly Leu Leu  
                   115                                  120                                  125  
 Phe Ser Gln Phe Leu Cys Val Ile Phe Phe Ile Ser Gly Gly Met Glu  
                   130                                  135                                  140  
 Phe Ile Leu Asn Ile Leu Tyr Glu Ser Tyr Gln Tyr Leu Pro Pro Gly  
                   145                                  150                                  155                                  160  
 Arg Thr Leu Leu Phe Asp Gln Gln Phe Leu Lys Tyr Ile Gln Ala Glu  
                                   165                                  170                                  175  
 Trp Arg Thr Leu Tyr Gln Leu Cys Ile Ser Phe Ser Leu Pro Ala Ile  
                   180                                  185                                  190  
 Ile Cys Met Val Leu Ala Asp Leu Ala Leu Gly Leu Leu Asn Arg Ser  
                   195                                  200                                  205  
 Ala Gln Gln Leu Asn Val Phe Phe Phe Ser Met Pro Leu Lys Ser Ile  
                   210                                  215                                  220  
 Leu Val Leu Leu Thr Xaa  
                   225                                  230

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Ser His Ser Leu Met Leu Phe Ile Thr Ile Trp Leu Lys Ala Ile Asn  
   1                                  5                                  10                                  15  
 Phe Ile Phe Ile

## (2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Lys Thr Gly Phe His Leu Tyr Glu Arg Glu Asn Arg Thr Ala Tyr Arg  
 1 5 10 15

Lys Glu Ile Thr  
 20

## (2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Gly Arg Ala Gly Cys Gln Lys Tyr  
 1 5

## (2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Asn Asn Ile Ile Ile Ser Ala Asp Cys Ala Leu Phe Val Phe Ser Phe  
 1 5 10 15

Leu Tyr

## (2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Lys Asp Asp Phe Asp Thr Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Val Asn Asn Phe His Ile Thr Ile Ser Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Thr Ile Phe Leu Cys Ile Asn Ala Ile Glu Ser Cys Phe Asn Arg Val  
1 5 10 15

Thr Asp Phe Cys Thr Ala Val Ser Gly Arg Trp Gly Asn Ser Cys Tyr  
20 25 30

Cys Gly

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Arg Val Ser Ser Gly Gly Gly Gly Tyr Cys Gln Gln Gly His Trp Phe  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Lys Arg Ala Tyr Lys Ser Gly Lys  
 1 5

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Ala Asp Ile Leu Phe Thr  
 1 5

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Arg Ser Arg Ile Met  
 1 5

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Ile Gln Pro Lys Ser Tyr His Ala Ile Ser Tyr Leu Cys Leu Phe Leu  
 1 5 10 15

Leu Leu Leu Cys Gln Tyr Phe Ser Gly Ala Thr Val Leu Trp Val Ser  
 20 25 30

Leu Trp Arg Ala Cys Gly Phe Phe Phe Asn Lys Met Val Met Gly Arg  
 35 40 45



Gly Asp Gly Phe Leu Tyr Arg Arg Trp His Thr Gly Leu Phe Phe Ser  
 50 55 60

Ile Leu  
 65

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Lys Ser Tyr Leu Lys Met Ser Lys Asp Asp Val Lys Gln Glu His Lys  
 1 5 10 15

Asp Leu Glu Gly Asp Pro Gln Met Lys Thr Arg Arg Arg Lys Cys Arg  
 20 25 30

Val Lys Tyr Lys Val Gly Val  
 35

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Leu Asn Leu Leu Asn Asn Leu Leu Arg  
 1 5

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Cys Val Ile Gln Arg Ile Leu Arg Phe Val Leu Ala Ile Ile Pro Pro  
 1 5 10 15

Ile Cys Gln Tyr His Ala Ser Trp Lys Lys Ala Val Met Leu Lys Leu  
 20 25 30

Thr Ile Leu Leu Thr Ser Leu Asn Ala Thr Ala Ser Pro Leu Leu Lys  
 35 40 45

Met Leu Ser Trp Pro Ala His Tyr Phe Leu Lys Trp Asn Ala Glu Ile  
 50 55 60

Lys Phe Leu Lys Arg Tyr Leu Asn Pro Leu Gln Pro Cys Tyr Val Trp  
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Ile Met Arg Ile Leu Pro Lys His His Lys Cys Phe Trp Tyr Ala Ser  
 1 5 10 15

Ser Gly His Cys Glu Gly  
 20

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Glu Gly Asn Ser Val  
 1 5

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Glu Thr Glu Asn Asn Arg Phe  
 1 5

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Pro Gly Thr Ser Thr Arg  
 1 5

(2) INFORMATION FOR SEQ ID NO:477:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Arg Ile Ile Lys Leu Asn Lys Ile Met Asp Trp Cys Val  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:478:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Met Asp Ser Asn His Ser Thr Pro Thr Met Ser Arg Trp Cys Ser Asn  
 1 5 10 15

Gln Leu Ser Tyr Glu Arg Gln Arg Cys Arg  
 20 25

(2) INFORMATION FOR SEQ ID NO:479:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Gln Arg Gly Arg Ile Leu Ala Ser Gln Pro Gln  
 1 5 10

009477 20947760

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

Gly Lys Arg Glu Ile Ala Ile Phe Phe Leu Lys Ser Pro Asp Cys Gly  
1 5 10 15  
Gly Asn Met Gln His Val Glu Lys Ile Ala Ala Met Arg Arg Leu Ser  
20 25 30  
Ser Tyr Tyr Arg Ser Ala Leu Gln Asn Asp Gly Gly Arg Leu Thr Leu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

Ile Ala His Pro  
1

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

His Arg Arg Arg Gly Gln Ala Asp Asp Glu Pro His Pro Glu Ala Cys  
1 5 10 15  
Arg Ser His Thr Ile His His Gln Ile Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

Arg Gln Asp Ile Thr Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

His Pro Val Gly Gly Lys Gly Asp Lys Lys Asp Gly Thr Arg Ile Phe  
1 5 10 15

Ile Thr Ala Gln Asn Thr Ala Ala Asp Asn Leu Tyr Arg Val Gly Asn  
20 25 30

Leu Val Asn Arg Ser Glu Gln His  
35 40

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Leu Arg Gln Ala Pro Arg Pro Gln Gly Cys His Cys Arg Ala Lys Gln  
1 5 10 15

Tyr Ala Tyr Ala Glu  
20

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Pro Gln Pro Tyr Lys Cys Arg Arg Leu Asn Arg Tyr Ala Leu Arg Leu  
165

009111"20911160

1 5 10 15

Arg Ile Gln Arg  
20

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

Ala Leu Ala Gln Thr Asp Asn Pro Leu Glu Ser Leu Pro Pro Gln Pro  
1 5 10 15

Ala Thr Ser Ala Val Arg Thr Ser Ala Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

Ala Gln Ser Asp Asp Arg Arg His Pro Gln Tyr Leu Met Ala Lys Pro  
1 5 10 15

Ala Ala Gln Arg Pro Gln Ile Thr Ser Leu Gln Arg Thr Ala Ser Ala  
20 25 30

Ile Gly Asn Pro Ser  
35

(2) INFORMATION FOR SEQ ID NO:489:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

Ile Arg Arg Phe Met Thr Thr Leu Ser Gly Leu Pro Lys Pro Phe Ser  
1 5 10 15

Leu Arg Ile Ser Arg Ile Glu Arg Ala Cys Leu Met  
166

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## (2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Glu Ser Met Ala Ile Asn Ile Thr Gln  
 1 5

## (2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

Thr Ala Ala Val Ala Thr Pro Gln Pro Ile Pro Pro Ser Ser Gly Ile  
 1 5 10 15

Pro Lys Trp Pro  
 20

## (2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

Phe Thr Gly Ile Phe Thr Ser Arg Pro Lys Asn Pro Ile Thr Ile Pro  
 1 5 10 15

Gly Leu Val Leu Ala Arg Pro Ser His Trp Phe Arg Ala Thr  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Lys Lys Arg Tyr Pro Ala Pro His Ser Ser Ala Arg Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Pro Thr Ala Leu Ser Ala Ser Ala Gly Ser Ile Leu Cys Ile Glu Arg  
1 5 10 15

Ile Met Tyr Pro Ala Phe His Arg Thr Ile Ile Thr Ser Thr Glu Thr  
20 25 30

Lys Pro Ala Ser Gln Asn Pro Cys Arg Thr  
35 40

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Cys Ala Ile Arg Ser Arg Arg Pro Glu Pro Leu Ser Cys Ala Ile Thr  
1 5 10 15

Gly Val Lys Ala Ser Ser Lys Pro  
20

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Pro Asn Lys Met Ala Gly Ser Arg  
1 5



(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

Arg Arg Gln Pro Cys Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Arg Tyr Ser Leu Pro Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:499:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

Arg Tyr Arg Arg Ile His Cys Gly Leu Tyr His Leu Arg Lys Asp His  
1 5 10 15

Arg Tyr Leu Asn Ala Asn Asn  
20

(2) INFORMATION FOR SEQ ID NO:500:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

Arg Ala Ser Leu Val Tyr Phe Cys Thr Tyr Ser Pro Phe Ile Leu Leu  
 1 5 10 15

Leu Tyr Glu Arg Leu Lys Ser Arg Arg Ser Gly Ser Gln Lys Lys  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Gln Gly Lys Phe Gln Ser Ile Val Ala Gly Tyr Tyr Tyr Phe Ser Ser  
 1 5 10 15

Glu Lys Thr Val Val Asn Gly Ala Leu Leu Ala Ser Cys Phe Ser Thr  
 20 25 30

Cys Tyr Cys Ala Glu Gln Phe Cys Phe Tyr Leu Phe Gln Glu Leu Lys  
 35 40 45

Ile Cys Leu Arg Gly Ser Tyr Arg Val Pro Arg Asn Trp Tyr Arg  
 50 55 60

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